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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:34:33 ; Search time 32.39 Seconds (without alignments)
256.730 Million cell updates/sec Perfect score: 658
Sequence: 10VOLOQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVTVSS 121
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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		Description		neavy chain v	g neavy chain	lbody Fab Jel	heavy chain pr	chain V	neavy chain	ıb Lead	neavy chain	neavy chain pr	neavy chain V	heavy chain v	heavy	heavy	gamma cha	Ig gamma-2a chain	heavy cha	heavy chain	heavy chain			heavy	heavy	heavy	heavy	Ig heavy chain pre	heavy chain	nti-glyc	φ	chain pr
SUMMARIES		QI	B22769	· c	553751	E30513	570546	MHMS18	PC4402	525175	31,007E	520643	B27563	730550	00000	2/4/20	00000	20000	A30577	PS0024	22420/	52631/	831930 810308	00000	20000	523041 737563	11 00 22	25007	2000	22 / C + O	CTCWUW	HVMST7
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æ	Query	Match						78.2					u,			75.2		•	, .	74.0	. 4		74.0	73.9	73.6	'n	•	· ~	73.1	3	ľ	4
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19 heavy chain v r ig heavy chain pre ig heavy chain v r
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477.5 477.5 477.5 478.5 478.7
33 332 332 332 332 332 332 332 332 332

## ALIGNMENTS

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Ig heavy chain precursor V region (B1-8) - mouse
N.Contains: Ig heavy chain precursor V region 186-2
Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Baccession: A90809; B90809; B27569; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A;Reference number: A90809; MuID:81234548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     igheavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20646
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A;Reference number: S20639
A;Reference number: S20646
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A; Residues: 1-139 <4B8>
A; Crossiues: 1-139 <4B3
A; Crossiues: 6B:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A; Accession: B90809
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A; Residues: 1-123 <LOS>
A; Cross-references: EMBL:X65001; NID:g52612; PIDN:CAA46134.1; PID:g52613
A; Cross-references: EMBL:X65001; NIP:g100; immunoglobulin V region; immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                           13;
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Pred. No. 2.7e-38;
9; Mismatches 11;
                                                                                516; DB 2;
No. 2.5e-38;
                                                                                                                                              6; Mismatches
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                      Score Pred.
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Local Similarity 79.2%;
les 99; Conservative 5
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nilarity 82.6%;
Conservative 6
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A; Residues: 1-123 <LOS>
                                                                                                                  Best_Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus () musculus () musculus () musculus () c;Species: Mus musculus () 
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A;Residues: 1-138 <KOF>
A;Cross-references: GB:M20835, NID:9196945; PIDN:AAA38847.1; PID:9196946
A;Cross-references: GB:M20815, NID:9196945; FIDN:AAA38847.1; PID:9196946
C;Super Perily: immunoglobulin V region; immunoglobulin homology
C;Super Revious: heterotetramer; immunoglobulin
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                                                                                                                                                                    Length 120;
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A;Residues: 1-116 <POK.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;Is-98/Domain: immunoglobulin homology <IMM>
                     immunoglobulin homology
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Pred. No. 1e-38;
3; Mismatches 10;
                                                                                                                                                                       DB 2;
                                                                                                                                                                       Score 527.5; DB 2
Pred. No. 2.2e-39;
                                                                                                                                                                                                                              4; Mismatches
                                  C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                              region;
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83.6%;
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85.1%;
                           immunoglobulin V
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Best Local Similarity 85.1
Matches 103; Conservative
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Best Local Similarity
Matches 102; Conserv
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A; Molecule type:

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If heavy chain V region - mouse

(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

(Species: Worselver)

(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

(Species: Musculus 1953

(Species: Musculus 1954

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A:MOLECULE type: mRNA
A:Residues: 1-141 < KAAA
A:Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Superfamily: signal sequence #status predicted <SIG>
F:1-19/Domain: signal sequence #status predicted <AIG>
F:34-117/Domain: immunoglobulin homology <IMM>
E:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:135-141/Region: Complementarity-determining 2
F:136-141/Region: C
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Pred. No. 3.3e-38;
8; Mismatches 12;
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Best Local Similarity 81.8%;
Matches 99; Conservative
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Best Local Similarity
Matches 97; Conserv
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                                                      hapt
A; Residues: 1-117-<1862>
A; Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt A; Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA R; Bruggemenn, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K. F. Briggemenn, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K. A; Ttele: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A; Reference number: A90971; MUID:84236026
                                                                                                                                                                                                                                                A; Molecule type: protein Molecule type: protein Molecules: 20-139 cDL>
A; Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch varion the mu chain
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J. Blochem. 122, 322-329, 1997
J. Blochem. 122, 322-329, 1997
J. File: Construction, bacterial expression, and characterization of hapten-specific sin A; Reference number: PC4402
A; Accession: PC4402
A; Molecule type: DNA
A; Residues: 1-287 < SUZ>
C; Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein C; Species: synthetic
C; Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C; Accession: PC4402
R; Syzuki, C:: Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem: 122, 322-329, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence fstatus predicted <SIG>
F;20-13/Porduct: 1g kappa chain V region (B1-8) #status experimental <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-124/Region: D segment
F;125-139/Region: J segment (JH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 7.4e+38;
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Best Local Similarity 81.0%; Pred. No. 3.4e-38;
Matches 98; Conservative 5; Mismatches 17
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81.0%;
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Matches 98;
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                                                                                                                           Ug heavy chain V region (35.8.2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23 Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C;Accession: C30560
F;Matsuda, T; Rabat, E.A.
J. Immunol. 142, 863-870, 1989
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1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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11 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWHHWVKQRPGGGLDWIGEINPSNGRINY
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                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M24270; NID:9195615; PIDN:AAA38371.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.6e-36;
3; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 498.5; DB :
Pred. No. 7.2e-37;
4; Mismatches 17
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es 95; Conserv
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A;Molecule type: mRNA
A;Residues: 1-118 <MA1
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Best Local Simi
Matches 97;
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Best Local Si
Matches 95;
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                                                                                                                                                                                                                                                                                             from autoimmune MRL mice react
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                                                                                                                                                                                       1g heavy chain V region - mouse
1g heavy chain V region - mouse
1g heavy chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Accession: $20643
R; Losman, M.; Fasy, T.M.; Novick, K.E.; Monestler, M.
R; Losman, M.; Fasy, T.M.; Novick, February 1992
A; Description: Relationships among antinuclear antibodies from autoimmune MRL min A; Reference number: $20639
A; Reference number: $20639
A; Accession: $20643
A; Accession: $20643
A; Accession: $20643
A; Residues: 1-122 < Loss
A; Coss-references: EMBL: X64998; NID: 952606; PIDN: CAA46131.1; PID: 952607
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Sate: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
C.Sate: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
C.Sate: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
R.Carmack, C.E.; Pincus, S.H.
J. Immunol. 137, 3983-3983, 1986
A.Title: Variable regions of antibodies to synthetic polypeptides. II. Analy
A.Title: Variable regions of antibodies to synthetic polypeptides. II. Analy
A.Reference number: A92812; MUID:87059009
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                   --- DYWGQGTTLTVS 134
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                   80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAREGPAG-
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Pred. No. 1.3e-37;
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78.8%;
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A; Residues: 1-117 <CAR>
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VTVS 122
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Search completed: April 13, 2001, 15:36:46
Job time: 133 sec
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C; Species: Mus musculus (house mouse)
C; Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C; Accession: S38950
C; Accession: S38950
A; Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha (A; Reference number: S38950; MuID:94128242
A; Reference number: S38950; MuID:94128242
A; Reference number: S38950; MuID:94128242
A; Reference number: S38950; MuID:94128242
C; Status: preliminary
A; Molecule type: protein
A; Residues: 1-246 <KLE>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: Immunoglobulin
C; Keywords: Immunoglobulin
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Submitted to the EMBL Data Library, January 1993
Abescription: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: $40295
A;Accession: $40295
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C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1.446/Product: Ig gamma-2a chalin #status experimental <MAT>
F;1.117/Domain; V-D-J region <VDJ>
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C:Date: 07-Apr_1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
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F:14Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental
                           61 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGT 115
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F;341-446/Domain: C3 region <CH3>
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A; Residues: 1-446 <KLE>
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on:

April 13, 2001, 15:35:47 ; Search time 21.32 Seconds (without alignments) 194.414 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-700-737-9 ... 658 658 1 QVOLQQPGAELVKPGTSVKL......DGWDYAIDYWGQGTSVTVSS 121

Scoring table:

93435 seqs, 34255486 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Que Mat	Lengt	DB	ID	Description
	514.5		139	<u> </u>	HOOT MOTION	
7	479.5	72.9	120		HVSO MOUSE	
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10	447	67.9	117	Н	HV12_MOUSE	8118
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77	445		117	-	HV04_MOUSE	SILE
		9. 79	117	П	HV13_MOUSE	Bus
T 4	441.5	67.1	118	-	HV51_MOUSE	Sil
15	441	67.0	117	-	HV49_MOUSE	Bus
97.	440	60.0	117	Н	HV10_MOUSE	mus
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9 6	•	9.00	117	-	HV41_MOUSE	P01811 mus musculu
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Ouery Match 78.2%; Score 514.5; DB 1; Length 139; Best Local Similarity 81.0%; Pred. No. 1e-44; Matches 98; Conservative 5; Mismatches 17; Indels 1;

P06326 homo sapien P01742 homo sapien P01768 homo sapien P01768 homo sapien P01772 homo sapien P01799 mus musculu P80421 homo sapien P01760 homo sapien P01804 mus musculu P01804 mus musculu P01796 mus musculu P01796 mus musculu	LT 1  JAOUSE STANDARD; PRT; 139 AA.  PO1751; PO1752;  21-JUL-1986 (Rel. 01, Last sequence update)  15-JUL-1986 (Rel. 01, Last sequence update)  16 HaRAY CHAIN WESTON B1-8/186-2 PRECURSOR.  WAS mountain to reach a sequence in a sequence in a sequence in antibodies: sometic mutation evident in a gamma 2a variable region.";  17-JUL-1986 (Rel. 01, M. A.  PARING ANTIBODIES TO THE B1-8 MU CHAIN MRNA MAS CLONED FROM A HYBRIDOMA ANTIBODIES)  1	al.  IG HEAVY CHAIN V REGION B1-8/186-2. FRAMEWORK 1. FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1. COMPLEMENTARITY-DETERMINING 2. COMPLEMENTARITY-DETERMINING 2. D SEGMENT. JH2 SEGMENT. BY SIMILARITY.
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                                                                                                             NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS
                                                                                                                                              QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                             20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGREEMIGRIDPNSGGTKY
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Pred. No. 2.7e-41;
7; Mismatches 22;
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23-OCT-1986 (Rel. 02, Last Sequence update)
24-UL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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illarity 75.2%;
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-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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                            Mushinski J.F.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION TEPC 1017. FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
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                                                                             "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984). PIR; A02033; HVMST7.
MEDLINE-84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R.,
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION S43 PRECURSOR.
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138 AA;
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Best Local Similarity
Matches 91; Conserv
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION 93G7 PRECURSOR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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                                                                                                                                                                                                                                 71.4%; Score 469.5; DB 1; Length 137; 73.4%; Pred. No. 3.1e-40; 1.1ve 7; Mismatches 17; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-82152818; Pubmed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                         17; Indels
                                                                                       HEAVY CHAIN V REGION S43
                                                                                                                      FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                  MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                             BY SIMILARITY.
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D SEGMENT.
JH2 SEGMENT.
send an email to license@isb-sib.ch).
                   EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region; Signal.
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137
137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                           Length 140;
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                 IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region; Antlarsonate antibody; Hybridoma.
                                                                                                                         22; Indels
1 19 1G HEAVY CHAIN V REGION 9
140 140 140 1514 MW; 25A4CBBE31DA5CE8 CRC64;
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                                                                                         71.3%; Score 469; DB 1;
73.6%; Pred. No. 3.6e-40;
tive 10; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                             21-JUU-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 36-65.
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                                                                                                      Similarity 73.6
39; Conservative
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Best Local Similarity 74.28
Matches 89; Conservative
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                                                                                    Query Match
Best Local Simi
Matches 89;
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P01747;
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HV06_MOUSE
ID HV06_MC
AC P01750;
DT 21-JUL-
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Signal.

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[mmunoglobulin V
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                                                                                                                                    "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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                                                                                                  STRATN=CS7BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV09_MOUSE STANDARD; PRT; 117 AA.
P01753; P11271;
P1 JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HRAVY CHAIN V REGION 186-1 PRECURSOR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                        RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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                                                                                                                                                                                                                                                                                                                                                                 Score 464; DB 1;
Pred. No. 9.2e-40;
3; Mismatches 6;
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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 QKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCA 97
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MEDLINE-81234548; Pubmed-6788376;
                                                                                                                                                                                                                             region; Signal.
19
117 IG F
                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.5%;
Best Local Similarity 90.6%;
Matches 87; Conservative 5
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                         InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region;
                                       Mus musculus (Mouse)
                                                                                                                                                                                                PIR; A02032; HVMS02
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117 AA:
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SEQUENCE
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HV09_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CSTEL/6;
MEDILINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                    COMPLEMENTARITY-DETERMINING 1.
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                              IG HEAVY CHAIN V REGION 186-1. FRAMEWORK 1.
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                                                                                                                                                                                                                                                                                   11; Indels
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                                                                                                                                                                                    12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 452; DB 1;
Pred. No. 1.4e-38;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-HUL-1999 (Rel. 38, PRECURSOR.
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                  68.7%;
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Best Local Similarity 85.77
Matches 84; Conservative
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region;
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117
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P01749;
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SEQUENCE FROM N.A.
                             NCBI_TaxID=10090;
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Zakut R., C
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P01748;
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                                                                                                                                                                                                                                                                                                   "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains."; Blochemistry 21:3415-3424(1982).

-I MISCELLANEOUS: THE SEQUENCE THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
-I MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                    Gaps
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                                                           1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                         MEDLINE-83075344; Pubmed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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              Score 451; DB 1; Length 117;
Pred. No. 1.8e-38;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%; Score 447; DB 1; Length 117; 71.1%; Pred. No. 4.6e-38; .ive 12; Mismatches 19; Indels
                                 Indels
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                                                                                                61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 98
                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV01_MOUSE STANDARD; PRT; 121 AA. 21-745; 21-101-1986 (Rel. 01, Created) . 1-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION MPC 11.
                                                                                                                                                            117 AA
             Match 68.5%;
Local Similarity 87.8%;
les 86; Conservative
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                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                Mus musculus (Mouse).
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P01756;
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Best Local Si
Matches 86;
             Query Match
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ID HV01_M
AC P01745,
DT 21-JUL,
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                               Matches
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Zakut R., Cohen J., Givol D.;
Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4440(1980).
1- MISCELLANGOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOWA THAT SECRETES IGG2B.
PIR; A02027, GVMS11.
InterPro; IRP003006; -
Pfam: PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 121 121
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MEDLINE-8124548; PubMed-6788376;
MEDLINE-8124548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24625-637(1981).
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                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-81053741; Pubmed-6253904;
Zakut K., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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-!- MISCELLANEOUS: THATS GERMLINE GENE BELONGS TO A SET OF CLOSE!
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%; Score 447; DB 1; Length 121; 69.4%; Pred. No. 4.8e-38; 1ve 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 121 121
SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAYY CHAIN V REGION 23 PRECURSOR.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA.
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PIRSCELL.

RELATED GENES

PIR; A02030; HVMS23;

A InterPro: IPR003006; -

AR Fam; PF00047; 1g; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.4'
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG-GYDGWDYAIDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARGYGYD----PFDVWGTGTTVTV 116
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84182519; PubMed=6201362;
MIDIDATOP R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
Dildatop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky R.;
"A V region determinant (idiotope) expressed at high frequency in B Imphotoytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR: MOD2040, MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-85999340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.1%; Score 441.5; DB 1;
70.5%; Pred. No. 1.6e-37;
iive 11; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-JUL-1999 (Rel. 38, Last annotation update)
IG-HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION AC38 205.12.
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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Cell 40:271-281(1985).
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                                                                                                                                                                      Aus musculus (Mouse)
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Matches 86; Conserv
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P06328;
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SEQUENCE
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HV49_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPGNGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEFRRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR; A26242: MHMSJ5.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                                                                                                                 Query Match 67.6%; Score 445; DB 1; Length 11' Best Local Similarity 84.7%; Pred. No. 7.2e-38; Matches 83; Conservative 2; Mismatches 13; Indels
       FRAMEWORK 2. COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                 12772 MW; C530F829C906F69B CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                         FRAMEWORK 3.
BY SIMILARITY.
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Pfam; PF00047; ig; 1.
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117 AA;
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HV51_MOUSE
ID HV51_MOUSE
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P01757;
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        EMBL; M13788; AAA38506.1; -.

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        PIR; A02035; MHMSB4.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q99xe9 mus musculu Q91177 mus musculu Q91181 mus musculu Q94xf0 mus musculu Q94x14 mus musculu Q94125 homo sapien Q91185 mus musculu Q94194 homo sapien Q91185 homo sapien Q91185 homo sapien Q94xf0 mus musculu Q91189 homo sapien Q94xf0 mus musculu Q94189 homo sapien Q94xf0 mus musculu Q94189 homo sapien Q959xf0 homo sapien Q959xf0 mus musculu Q94xf0 mus musculu Q94xf0 mus musculu Q95x78 homo sapien homo sapien homo sapien homo sapien Description Q9u193 h Q9u190 h Q9y509 h SUMMARIES 090XE9 090L17 091L81 090XF0 090L104 091L12 091L92 091L93 091L83 091L83 091L83 091L83 091L83 091L83 091L83 091L83 091L83 Q9UL93 Q9UL90 Q9Y509 ū DB Length Query Match 1 Score 473 464.5 462.5 459 458.5 414.5 414.5 414.5 390 390 386.5 353.5 353.5 349 323 317 313.5 3 6 7 111 112 113 114 118 118 119 Result

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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=DBA/2;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF206029; AAF69327.1; -.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
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79.38;
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Best Local Similarity 79.3
Matches 88; Conservative
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Best Local Similarity
Matches 88; Conserv
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Q9JL77
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Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P. Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric IGGZ/G4 constant regions block human leukocyte binding to porcine endochelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKGKATLTYDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDK----DYYFDYWGQGTTLTVS 116
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.8%; Score 459; DB 11; Length 117; 72.7%; Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ22311; CAB65236.1; -.
INTERPRO; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13060 MW; D816AD0858A47E4C CRC64;
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                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
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117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.8'
Best Local Similarity 72.7'
Matches 88; Conservative
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PRELIMINARY;
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SEQUENCE 117 AA; 13
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PFAM; PF00047; 19; 1.
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DB 11; Length 118;

Score 458.5;

69.78;

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endothelial cells.";
Submitted (NOV-1996) to th
EMBL; U78799; AAD00291.1;
INTERPRO; IPR003006;
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TVSS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; Malkiel S., Liao L., Cunningham M.W., Diamond B.; Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acctyl-glucosamine antibodies from mice with autolumune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF206031; AAF69329.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C;
Mueller J.P., Glannonl M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Mueller J.B., Evans M.J.;
Matls L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
                                                                                                                                                                                           61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGWDYAIDYWGQGTSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                              1 OVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                     1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 LTVDISSSTAYMQLSSLTSEDSAVYYCAR-GGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 109;
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12118 MW; FF65E441BBF936A6 CRC64;
                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.2%; Score 442.5; DB 1
Best Local Similarity 76.1%; Pred. No. 5.8e-39;
Matches 86; Conservative 8; Mismatches 14
71.8%; Pred. No. 1.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA.
                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                        89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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109 AA;
Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                                               115 TVSS 118
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NON_TER
SEQUENCE
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09JL75
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGKATLITVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                24; Indels
the EMBL/GenBank/DDBJ databases
                                                                                                                                 4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                   Score 437; DB 11;
Pred. No. 2.4e-38;
8; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
INTERPRO; IPR003006; -.
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                                                   FRAM: PF00047; ig; 1.

NON_TER 1 1

NON_TER 117 117

SEQUENCE 117 AA; 13122 MW;
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70.2%;
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**Q9UL94** 

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10 ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT
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MEDLINE=98277139; PubMed=9614934;
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                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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NON_TER
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ID Q9UL95
AC Q9UL95;
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                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JON 2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDG-WDYAIDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TIEMBLIEL 15, Created)
01-0CT-2000 (TIEMBLIEL 15, Last sequence update)
01-0CT-2000 (TIEMBLIEL 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                 62.9%; Score 414; DB 4; Length 119;
65.6%; Pred. No. 6.1e-36;
Live 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                      13205 MW; 13E64F5345F4A16E CRC64;
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EMBL, ARD$5020, ARD$6256.1; -.
INTERPRO: IPRO03006; -
PFAM: PF00047; 19; 1.
                 119 AA
                 PRT;
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                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 65.69
Matches 80; Conservative
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nes 79; Conservative
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                   PRELIMINARY;
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110 AA;
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SEQUENCE
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STRAIN=BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01.-UNV-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
69
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                                                         61
                                 2 ELVKPGASYKISCKASGYTFSNSWNWWYKLRPGQGLEWÏGRIYPGDGDAYYNGKFKGKAT
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNGELOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                               62 LTADKSSSTAYMQLSSLTSVDSAVYFCAR---SNWDVRFAYWGQGTLVTVSA 110
                                                                                                                             70 LTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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60.0%; Pred. No. 2.1e-33;
iive 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AA; .13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 2.1e-33;
ches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
INTERPRO; IPR003006; -.
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150 AA;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                      01-JUN-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                    Gaps
                                                                                                            9 AELVKPGTSVKLSCKGYGYTFTSYMMHWVKQRPGGGLEWIGEIDPSESNTNYNQKFKGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 QPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                    4,
                                                                                                                                         69 TLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                     54.2%; Score 356.5; DB 4; Length 116; 60.3%; Pred. No. 6e-30; 1.ve 16; Mismatches 29; Indels 1
                                                                Length 109;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BEDILNE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                 Indels
                              DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        116 116 116 116 116 AA; C8F9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                          Query Match 58.7%; Score 386; DB 11; Best Local Similarity 64.6%; Pred. No. 4.6e-33; Matches 73; Conservative 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035025; AAD56261.1; -
INTERPRO; IPR003006; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298
                                                                                                                                                                                                                                     Created)
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                              109 AA; 11944 MW;
                                                                                                                                                                                                           Q9UL89
Q9UL89;
01-MAY-2000 (TFEMBLFEL 13, 0
01-MAY-2000 (TFEMBLFEL 13, 0
01-JUN-2000 (TFEMBLFEL 13,
EMBL; AF206021; AAF69319.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 60.38
Matches 70; Conservative
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01-MAY-2000 (TrEMBLrel, 1:
01-CCT-2000 (TrEMBLrel, 1:
CN 8 SCFV.
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STRAIN=BALB/C; TISSUE=SPLEEN;
shinobhara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYYGHS---AYWGGGTTVTVS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-99332155; PubMed-9657749; Jacquemin M.G., Vander Elst L.P.L.; Mechanism and kinetics of factor VIII inactivation: study with an ING4 monoclonal antibody derived from a hemophilia A patient with inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Indels
                                                                                                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AB036341; BAA88633.1; -. HSSP; P01607; IRRI. INTERPRO; INTERPRO; PFAM; PF000047; ig; 2. SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
16031 MW; 563D164AB22802D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
IGG VH PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.5%; Score 352; DB 4;
57.0%; Pred. No. 2.4e-29;
iive 14; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.7%; Score 353.5; DB 55.4%; Pred, No. 4e-29; ive 16; Mismatches
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EMBL; AJ224083; CAA11829.1; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.4%
Matches 67; Conservative
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Search completed: April 13, 2001, 15:39:52 Job time:  $264\ \mathrm{sec}$ 

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; Search time 57.59 Seconds
(without alignments)
120.103 Million cell updates/sec
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1 QVQLQQPGAELVKPGTSVKL......DGWDYAIDYWGQGTSVTVSS 121
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(SIDSI/gcgdata/geneseq/geneseqp/AA1980_DAT:*

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390729 seqs, 57163235 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mus sp

		Description	Murine Act-1 heavy	Consensus protein	Protein sequence o	Heavy chain of a h	Anti-DNA antibody	Anti-EGFR antibody	Anti-Fas MAb HFE7A	Mouse anti-Fas ant	Murine anti-Fas an	B-cell lymphoma CH	Anti-EGFR antibody
	£	T.	W53815	W53816	W53818	W53813	W07436	R79863	W83041	B14747	W90897	R84555	R79861
	9	9 :	19	19	19	13	18	16	19	21	21	16	16
	Query	1113 611	140	144	137	180	119	119	464	464	464	122	119
øp	Query	111111111111111111111111111111111111111	100.0	100.0	98.3	86.5	81.8	81.5	79.5	79.5	79.5	79.1	79.0
	91000	2010	658	658	646	569	538	536	523	523	523	520.5	520
	Result		-	7	m	4	Ŋ	9	7	<b>&amp;</b>	6	10	11

MAb 55.1 heavy cha MAb 55.1 heavy cha	Murine antibody he	pRAS111 between H1	Scrv pRAS107 and p	ScFV pRAS110 and p	ScFV pRAS108 and p	Fusion protein pNG	Plasmid pNG4/55.18	Murine anti-CD18 A	Lead binding MAb 8	Sequence encoded b	Anti-hepatitis B h	Mouse-human chimae	Chimeric anti-hepa	Human anti-hepatit	Human anti-hepatit	Human anti-hepatit	Chimeric anti-hepa	ScrvB18 construct.	ScFvB18 construct	ScFvB18 construct	ScFvB18 construct	ScrvB18 construct	ScrvB18 construct	Single chain antig	Single chain antig	Anti-tobacco mosaí	VH425 antibody clo	Mouse antibody hea	ScFvB18 construct	ScFV pRAS109 and p	Murine 15B8 heavy	ScFv(FWP51). Synt
5 1	9 18	15	3 IS	~	12	8 20	3 20	0 15	9	80	18	18	5 18	2 19	19		20	5 13	5 13	5 13	9	5 13	2	3 18	3 18	5 16	0 13	7 17	6 13	5 15	9 21 Y9	0 16
0 0	78.8	78.6	78.6	78.6	9.87	9.82	78.6	78.5	78.0	77	7.77	7.77	7.77	77.7	77.7		7.77	77.6	9.	77.6	77.6	77.6	77.6	77.4	77.4	77.4	77.2	77.1		77.0	76.7	76.4
12 13											24	22	56	27	28	29																

## Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease. Murine Act-1 heavy chain variable region. W53815 standard; Protein; 140 AA. (first entry) 14-JUL-1998 W53815; RESULT W53815

ALIGNMENTS

/note= "signal peptide" "mature protein" Location/Qualifiers 1..19 97WO-US13884 20..140 /note= "r WO9806248-A2. 06-AUG-1997; 19-FEB-1998 Key Peptide Protein 

96us-0700737.

15-AUG-1996;

(LEUK-) LEUKOSITE INC

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Misc-difference
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                                             Peptide
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                                                                                                                                 The present sequence represents the heavy chain varaible region of murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadcAm-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadcAm-1, which is present of high endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKGKATLIYDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus protein sequence of the murine variable heavy chain region.
                                                                                                                                                                                                                                                                                                                                                                  20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewlgeidpsesntny 79
                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                  .
0
                                                                  Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                          Length 140;
   Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by TRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by TGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-
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                                                                                                                                                                                                                                                                                                        Score 658; DB 19;
Pred. No. 3.4e-47;
  Ponath PD,
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W53816 standard; Protein; 144 AA.
   Newman W,
                                                                                                                  English.
                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 121; Conservative
                                                                                                                Claim 27; Fig 9; 145pp;
   Jones ST,
                                   WPI; 1998-159172/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 5
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                                               N-PSDB; V20078
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  Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 s 140
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 S 121
                                                                                                                                                                                                                                                                            Seguence
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The present sequence represents the consensus amino acid sequence comprising the variable region of murine Act-1 antibody determined from several independent mouse heavy chain variable region clones. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Variable regions were amplified from DNA encoding Act-1 using degenerate PCR primers V20079-82. The degeneracy of the PCR primers produced several different sequences, of which the present sequence is a consensus sequence. The present sequence was used to construct chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte as infiltmation of tissues, e.g. for treating inflammatory diseases such a collision and diseases. The immunoglobulin can also be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ringler DJ;
                                                         /note= "not specified, encoded by YTC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CDR3"
131..141
/note= "framework region 4"
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                                                                                                                                                                                                                                "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "framework region
                                                                                                                                                                      "mature protein"
'note= "encoded by ATY"
                                                                                                                /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                             "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newman W,
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                                                                                                                                                                                                                                                                                         "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                   "CDR2"
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                                                                                                                                           20..144
/note= "m
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/note= ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118..130
                                                                                                                                                                                                                                                                                            /note= 755..68
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N-PSDB; V20085.
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                           Misc-difference
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Saldanha J;
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NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVT 118 

(first entry)

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20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewlgeidpsesntny 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; Act-1 antibody; human alpha4-beta7 integrin; Makscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain of a humanised murine Act-1 antibody.
                                                                                                                                                                                                                                                                                                                      W53813 standard; Protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9806248-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin blinding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The present sequence was used to construct chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infilitration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequence of murine variable heavy chain region of clone H2B#34.
                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewigeidpsesntny
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diabetes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma, graft versus host disease and sarcoidosis
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                                                                                                                                                                                                                                                                                                                                                                                                       W53818 standard; Protein; 137 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-159172/14.
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                                                                                                                                                                                                                                                  140 s 140
                                                                                                                                                                                     S 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                       80
                                                                61
                                                                                                                                                                                     121
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1..19 /note= "signal peptide" 20..180 /note= "mature protein" Location/Qualiflers

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The present sequence represents the heavy chain of humanised murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4 beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing all algand for alpha4-beta7. It can be used for inhibiting leukocyte Infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    integrin
diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 180;
                                                                                                                                                                                                                                                Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis, asthma, graft versus host disease and sarcoldosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 569; DB 19;
Pred. No. 8.8e-40;
                                                                                                                                                                                                                                                Ponath PD,
                                                                                                                                                                                                                                                Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Fig 11; 145pp; English.
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85.1%;
                                                                  97WO-US13884.
                                                                                                                           96US-0700737
                                                                                                                                                                                                                                                Jones ST,
                                                                                                                                                                                    (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                                                                                                     WPI; 1998-159172/14.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V20076
                                                               06-AUG-1997;
                                                                                                                        15-AUG-1996;
19-FEB-1998
                                                                                                                                                                                                                                             Bendig MM,
Saldanha J;
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98.2%; Score 646; DB 19; 100.0%; Pred. No. 3.2e-46; ive 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 118; Conservative

Gaps

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Length 137;

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61 ngkfkgkatltvdkssstaymqlssltsedsavyycakgrlry----famdywgrgtsyt 116
                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-epidermal growth factor receptor (EGFR).single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                     9
which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAD can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephrits and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder. The sequence was derived by aligning homologous anti-DNA MAD, whose sequences have been published, as well as several MAD of other specificities obtained from a database search.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
                                                                                                                                                                                                                                                                                     1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-EGFR antibody heavy chain variable region (Clone L3 11D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-EGFR antibodies and single chain Fv antibody fragments obtained from phage-antibody libraries, useful for diagnosis
                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                Score 538; DB 18; Leus...
Pred. No. 2e-37; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guessow D;
Rosell E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blasco F,
                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piulats J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R79863 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 53; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kettleborough AC, Mitjans F,
                                                                                                                                                                                                                          81.8%;
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94EP-0104160.
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                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy of tumours
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                              119 AA;
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                                                                                                                                                                                                                                            Best Local Sir
Matches 105;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                            Query Match
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        0;
                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the heavy chain variable region of the group 9f11 putative consensus anti-DNA monoclonal antibody (MAb),
                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain; variable region; anti-DNA; monoclonal; antibody; 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease; consensus; putative.
                                                                                                                                                                                                                                                                                                                                                                      Anti-DNA antibody 9f11 group heavy chain variable region.
         10; Indels
         Mismatches
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/label= framework_III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= framework_II
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/label= framework_I
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                                                                                                                                                                                                                                                                             W07436 standard; Protein; 119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50..66
/label= CDR_II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31..35
/label= CDR_I
36..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US07113.
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                                                                                                                                                                                                                                                                                                                                            (first entry)
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           Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swanson PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-011854/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T43805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                            12-AUG-1997
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                                                                                                                                                                  s 121
                                                                                                                                                                                                s 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                             W07436;
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vitro and in vivo. They may also be used in a pharmaceutical compostion for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. (See T04011-T04026 and
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                       1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWLGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                               HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                          Score 536; DB 16;
Pred. No. 3e-37;
4; Mismatches 12;
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'label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label- Variable
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/label= Constant
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/note- "claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Fas MAb HFE7A heavy chain.
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/label- CDR_H2
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/label- CDR_H1
                                                                                                                                                                                                            81.5%;
85.1%;
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                                                                                                                                                                                                                                              Matches 103; Conservative
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                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                             119 AA;
                                                                                                       R79858-R79873)
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                                                                                                                                             Sequence
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                                                                                                                                                                                                          Query Match
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W83041
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This is the amino acid of the heavy chain of murine anti-human Fas chain was obtained from HFF7A-secreting hybridoma (FERM BP-5828)

Chair bodies are capable of inducting apoptosis in abnormal cells antibodies are capable of inducting apoptosis in abnormal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, softenem, pernitatious anaemia, Addison's disease, selectederma, Goodpasture syndrome, crohn's disease, themmatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia carthritis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergles, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 qvqlqqpgaelvkpgasvklsckasgytftsywmqwvkqrpgqglewlgeldpsdsytny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                              Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference Example 4; Page 187-188; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.5%; Score 523; DB 19;
83.5%; Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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98AU-0059701
                                                      97JP-0276064
                                                                                     97JP-0082953.
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Best Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                                                          (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                    WPI; 1998-543440/47.
N-PSDB; V71029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 AA;
30-MAR-1998;
                                                      08-OCT-1997;
                                                                                                                25-JUN-1997;
                                                                                                                                                                                                                                 Akio S, Hić
Masahiko O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 - NOV - 2000
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA.

To a humanised version of HFETA containing identical CDRs or a humanised version of HFETA containing identical CDRs or a humanised version of HFETA containing identical CDRs interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
             Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                      Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 nqkfkgkatltvdtssstaymqlssltsedsavyycarnrdysnnwyfdvwgtgttvtvs 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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complementarity determining region; CDR; human Fas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 523; DB 21;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                    (SANY ) SANKYO CO LTD
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Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                    JP2000169393-A.
                                                                                                                                                                                                                                                                                                                                                          N-PSDB; A72108
                                                                                                                                                                                                                             30-SEP-1999;
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This invention describes a novel humanized anti-Fas antibody-like conceule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ingenue (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents contained in the products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunodilatory, dermatological, immunosupressive, thyromimetic, antirhemmatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity, induce containt and hepatropic activity, systemic inhibition of ligand binding (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic contains associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft conemia, Addison's disease, rheumatoid arthritis, graft conemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cone inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in curvine antive ligand, do not induce liyer disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents and murine antibody HFETA heavy chain described in the mative ligand, do not induce ligand eriver disease, and have reduced risk of a murine anti-normal antibody HFETA heavy chain described in the
                dermatological; immunosuppressive; thyromimetic; antitrheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; nephrotropic; numanized; apoptosis; systemic luues crythematosus; HEFA; Hashimoto disease; rheumatolod arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; antity; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example reference 4; Page 100-102; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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83.5%; Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-0276881.
98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; A11546
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1998;
30-SEP-1998;
                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serizawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
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Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;

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ò g à R84555;

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RESULT R84555

Mus sp.

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Anti-epidermal growth factor receptor (EGFR) single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in vitro and in vivo. They may also be used in a pharmaceutical composition for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. (See T04011-T04026 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single chain antibody, antibody, epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-EGFR antibodles and single chain Fv antibody fragments - obtained from phage-antibody libraries, useful for diagnosis and
                                                                                                                    Anti-EGFR antibody heavy chain variable region (Clone L2 12B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%; Score 520; DB 16;
81.8%; Pred. No. 6.1e-36;
iive 6; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                , Bendig MM, Blasco F,
Mitjans F, Piulats J,
                              Ą.
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                            R79861 standard; Protein; 119
                                                                                                                                                                                                                                                                                                                                     94EP-0118970.
                                                                                                                                                                                                                                                                                                                                                                                   (MERE ) MERCK PATENT GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-336972/43.
                                                                                                                                                                                                                                                                                                                                                                                                                Ansell KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy of tumours
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nes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Kettleborough AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 AA;
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                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                         WO9525167-A1
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17-MAR-1994;
                                                                                      02-JUL-1996
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Matches 99;
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RESULT
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                                                                                                                                                                                                                                                                                                Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic; B-cell lymphoma; CH12; IgM.
      NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYAIDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The heavy chain variable region amino acid sequence (given in R84554) of monoclonal antibody SCH94.03 shows extensive sequence similarity with the corresp. sequence (R84555) of the Igm produced by B-cell lymphoma CH12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases the CNS.
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Pred. No. 5.7e-36;
4; Mismatches 18; Indels 1:
                                                                                                                                                                                                                                                                 B-cell lymphoma CH12 IgM heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 40; 63pp; English.
                                                                                                                                                                         R84555 standard; Protein; 122 AA
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81.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodriguez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYO-) MAYO FOUNDATION.
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                                                                                                                                                                                                                                     02-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                           WO9530004-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1995;
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Matches 9
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MAD 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (094037) and light (094036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 qvq1qqpgaelvkpgasvq1sckasgytftgywihwvkqrpgqglew1gevnpstgrsdy 79
binding structure; complementarity determining region; CDR; colorectal cancer; tumor associated antigen; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
 call, colorectal cancer; tumor-associated antigen; hybridoms; monoclonal antibody; MAD; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                           Paterson DS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 520; DB 16;
80.2%; Pred. No. 2.4e-35;
live 10; Mismatches 14;
                                                                                                                                                                                                               97-98"
                                                                                                                                                                                                                                                                                                                                                                                                                           Hall SM,
                                                                                                                                                                                                 /label= Mat_protein
/note= "claim 3, page
                                                                                                                                                  1..19
/label= Sig_peptide
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig.15; 121pp; English.
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                                                                                                                                                                                                                                                                                                              94WO-GB02610.
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/label= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-215262/28
                                                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; 094037
                                                                                                                                                                                                                                                                                                              29-NOV-1994;
                                                                                                                                                                                                                                                                                                                                             03-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                          03-DEC-1993;
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                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An antigen binding structure is based on the CDRs (given in R76078-84) of the heavy (R76085) and light (R76086) chains of MAb 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CA55.1. It is optionally humanized and in the form F(ab') 2; Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monochonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen binding structures containing CDRs recognising the CA55.1 antigen – produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Hall SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 97-98; 121pp; English.
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                                                                                                                                                                                                                                                                                                94WO-GB02610.
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                                       (first entry)
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Best Local Similarity 80.2%
Matches 97; Conservative
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Wright AF;
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                                                                     55.1 heavy chain
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03-DEC-1993;
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Sequence

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SXEXEX XEXEX

121

Rose MS, Blakey

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Gaps

Length 464; Indels us-08-700-737-9.rag

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                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide sequence comprises a consensus sequence of murine heavy chain variable regions (VH) selected on the basis of identity to the VH region (see W27120) of monoclonal anti-idiotype antibody 11010. The sequences were obtained from a GenBank database search. A VL consensus (W27121) was also produced. 11010 has at least 18 departures from the consensus sequences (7 in the light chain and 11 in the heavy chain). B Occur within CDRs and 10 outside CDRs. 11010 polypeptides and polynucleotides can be used in vaccines and pharmaceutical compositions for the treatment of human milk fat globule-associated diseases such as breast
                                                                                                                                                                                                                                                                                                                                        Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours, especially breast cancer
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E
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Pred. No. 8e-36;
5; Mismatches 14; Indels 3;
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      Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine.
                                                                           "complementarity determining region 1"
                                                                                                                             note- "complementarity determining region 3"
                                                                                                    'note= "complementarity determining region
                                                                                                                                                              /note= "unspecified amino acid residue"
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                                                                                                                                              /note= "unspecified amino acid residue"
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                                                   .ocation/Qualiflers
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                                                             Ji..js
/label- CDR1
                                                                                   50..66
/label- CDR2
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95US-0575762.
96US-0591965.
                                                                                                                      CDR3
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Best Local Similarity 81.8%;
Matches 99; Conservative :
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                                                                                                          99..107
/label-
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                                                                                                                                     Misc-difference
                                                                                                                                                                      Misc-difference
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20-DEC-1995;
26-JAN-1996;
                                Mus musculus
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Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus;
Penton fibre; Ad5; Fusion sites; PCR; polymerase chain reaction.
                                                                                                                                                                                                                                                  1..42
2016 pelB leader peptide
23..142
/label- heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= (G4S)3 Linker
158. 269
/label= Light chain variable region
                                                                                                                                                                                                Location/Qualifiers
1..269
/label= Single chain Fv fragment
                                                                                         pRAS111 between HindIII and EcoRI sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
R54756 standard; Protein; 269 AA.
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/label- VL CDR 1
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/label- VH CDR 2
89..120
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/label= VL CDR
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/label- vH FR2
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/label- VH FR1
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/label- VL FR3
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/label= 1
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N-PSDB; Q64817.
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                                                                                                                                                                  Synthetic.
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R54756 showes an ScFv (VH and VL partner domains are linked via a flexible oligopeptide) between the HindIII and EcoRI sites of pRASI11. The 130 bp HindIII-PstI fragment of pRASI11 (Q64806) was used to replace the corresponding fragment of pRASI11 (Q64817), to qenerate pRASI8 This generates a NIP-reactive ScFv (NIP = 4-hydroxyl-3-iodo-5-nitrophylacetic acid) with a BgIII cloning site immediately downstream of the pelB leader, suitable for inserting fragments of Ad5 fibre.

The invention is concerned with the fusion of an ScFv with the Ad5 fibre that the fusion sequence can be used to target cells for
         Virus with modified binding molety specific for the target cells - used to deliver genes for gene therapy and cancer treatment \,
                                                                               Example 2; Page 69-70; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                              gene therapy.
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1; 61 NOKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120 1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60 23 qvq1qqpgaelvkpgasvklsckasgytftsywmhwvkqrpgrglewigridpnsggtky 82 Gaps 1; Query Match

78.6%; Score 517.5; DB 15; Length 269;
Best Local Similarity 81.8%; Pred. No. 2.2e-35;
Matches 99; Conservative 4; Mismatches 17; Indels 1; δ g ò q

269 AA;

Sequence

142 s 142

121 S 121

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Search completed: April 13, 2001, 15:35:37 Job time: 116 sec

Sequence 3, Appliseduence 2, Appliseduence 2, Appliseduence 12898, Appliseduence 5, Appliseduence 3, Appliseduence 10336, Appliseduence 10336, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 1117, Appliseduence 1167, Applisedu

US-09-815-108-3 US-09-815-108-2 US-09-815-108-2 US-09-815-108-2 US-09-813-742-3 US-09-813-742-3 US-09-813-742-3 US-09-809-391-754 US-09-739-449-10936 US-09-739-449-10936 US-09-739-449-11717 US-09-509-031-3 US-09-509-031-3 US-09-509-031-3 US-09-509-031-3 US-09-509-031-3 US-09-509-031-8 US-09-739-449-9917 US-09-739-449-9917 US-09-739-449-9117

ALIGNMENTS

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APPLICANT: Newman, Roland A. APPLICANT: Newman, Roland A. APPLICANT: Reff, Mitchell E. APPLICANT: Reff, Mitchell E. APPLICANT: Rastetter, William H. TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND TITLE OF INVENTION: RADIOGABELED ANTEGODIES TO HUMAN B LYMPHOCYTE RESTRICTED TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: PILLSBURY WINTHROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: PILLSBURY WINTHROP
1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08475815A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Darrell R. APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 140 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-815A-11
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STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07
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US-08-475-815A-11
STREET:
228
332
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                                                                             April 13, 2001, 17:35:04; Search time 4.45 Seconds (without alignments) 47.200 Million cell updates/sec
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Sequence 2, Appli
Sequence 12328, A
Sequence 12328, A
Sequence 11339, A
Sequence 11223, A
Sequence 2, Appli
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Sequence 2, Appli
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6, Appli
4, Appli
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28, Appl
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4, Appli
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 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-733-449-11638
US-09-386-658-4
US-09-814-950-4
US-09-814-950-2
US-09-739-449-12328
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US-09-782-504-4
US-09-509-031-11
US-09-509-031-6
US-08-475-815A-7
US-08-475-815A-7
US-09-193-562D-28
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US-09-815-108-15
US-09-815-108-17
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Perfect score:
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23522-0157

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CITY: Seattle
STATE: Washington
; OTHER INFORMATION: DESCRIPTI
; OTHER INFORMATION: sequence
US-09-509-031-16
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOLDES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                         61 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVHLQQSGPELVRPGASVKISCKTSGXVFSSSWMNWVKQRPGGGLKWIGRIYPCNGNTNY 79
                                                                                                            20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79
                                                             Gaps
                                                                                          1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNINY 60
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                          Score 486; DB 4; Length 140; pred. No. 1.8e-44; 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Erlanger, Bernard
APPLICANT: Erlanger, Chen, Bi-Xing
TITLE OF INVENTION: ANTHRODIES SPECIFIC FOR FULLERENES-
FILE PEPERBANCE: 0575-54182/JPW/SHS/WVM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEO ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.7%; Score 426; DB 5; 67.8%; Pred. No. 2.6e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Petentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.509-509-031-16
Sequence 16, Application US/09509031
GENERAL INFORMATION:
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                                  73.98;
76.98;
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                                                                    Conservative
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; ORGANISM: mouse [murine]
US-09-386-658-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Watches 82; Conserv
                                                1 Similarity
93; Conserv
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                                    Query Match
                                                         Local
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                                                                                                                                                                                                                                                                                          59 NYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVT 118
                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNT 58
                                                                                                                                                              Gaps
Description of Artificial Sequence:ccMTLgL protein
                                                                                                                                                                                                                                 8
                                                                                                               Length 482;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 'Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,504
FILING DATE: 12-Feb-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Law Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09782504
Sequence 4, Application US/09782504
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Helistrom, Karl Erik
Bruce, Kim Folger
Schreiber, George J.
Siegall, Clay
McAndrew, Stephen
TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.8%; Score 242; DB 5; 1
Best Local Similarity 47.9%; Pred. No. 4.8e-19;
Matches 58; Conservative 24; Mismatches 31;
                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMÉ: ROSEDMAN Ph.D., Stephen J. REGISTRATION NUMBER: 43,058 REFERENCE/DOCKET NUMBER: 840065.405D3
                                                                                                                    ; Score 278.5; DB 5; Pred. No. 1.9e-22; 27; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARCINOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                      Query Match 42.3%;
Best Local Similarity 43.9%;
Matches 54; Conservative 27
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                                                               61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                   APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, GATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.11
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APPLICANT: Suess, Garage M.
APPLICANT: Tarilnton, David M.
APPLICANT: Tarilnton, David M.
APPLICANT: Tarilnton, Caralytic ANTIBOIDES AND A METHOD OF PRODUCING SAME FILL OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILL ERFERENCE: 13474.
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILLNG DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
LENGTH: 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VOLOOPGABLVKPGTSVKLSCKG----YGYTFTSYMMHWVKQRPGQG----LEWIGEID 52
QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Kappa
OTHER INFORMATION: protein sequence
US-05-509-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 155;
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16.3%; Score 107; DB 5;
Best Local Similarity 27.3%; Pred. No. 2.4e-05;
Matches 35; Conservative 19; Mismatches 46
                                                                                                                                                                                                                                                    Sequence 11, Application US/09509031 GENERAL INFORMATION:
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; Sequence 6, Application US/09509031
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-509-031-11
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APPLICANT: SUGSS, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TILLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                 53 PSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 111
                                                                                                                                                                                                                               2 VQLQQPGAELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 52
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; OTHER INFORMATION: Description of Artificial Sequence: TLHL protein; OTHER INFORMATION: sequence
US-09-509-031-6
                                                                                                                                                                                                                                                                        32 VMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNY-LAWYQQKPGQPPKLLIYW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: CATAB-TEV OTHER INFORMATION: protein sequence US-09-509-031-4
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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Newman, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
                                                                                                                                             Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.3%; Score 107; DB 5; Length 495;
Best Local Similarity 27.3%; Pred. No. 9.1e-05;
Matches 35; Conservative 19; Mismatches 46; Indels
                                                                                                                                16.3%; Score 107; DB 5; Length 34 27.3%; Pred. No. 5.9e-05; Live 19; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
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ORGANISM: Artificial Sequence
                                                                                                                             Query Match
Best Local Similarity 27.38
Matches 35; Conservative
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| 134 GQGTKLEI 141
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58 TNYNQKFKGKATLIYDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSV 117
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                                                                                                                                                                                                                                                                                                                                         156 KA----DVKSLVWYVPENFEEAGYKVPESMEDLLKLTDQIVADGGTPWCIGLGSGGATGW 211
                                                                                                                                                                                                                                                                                              -----QLSSLTSE---DSAVYYC---ARGGYDGW 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels 33; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pauli, Benedicht U. APPLICANT: Pauli, Benedicht U. APPLICANT: Pauli, Benedicht U. TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules FILE OF INVENTION: ACTIVATED CURRENT APPLICATION NUMBER: US/09/193, 562D CURRENT FILING DATE: 1998-11-17 PRIOR PLING DATE: 1997-11-17 NUMBER OF SEQ ID NOS: 47 SEQ ID NOS: 47 LENGTH: 214
                                                                                                                                                                                                       9 AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNTNYNQKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 914;
                                                                                                                   Length 442;
                                                                                                                     10.6%; Score 69.5; DB 5;
25.0%; Pred. No. 0.58;
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APPLICANT: SMITHKLINE BEECHAM P.1.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: PCT/US01/09226
CURRENT APPLICATION NUMBER: 60/192,158
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR PELING DATE: 2000-03-27
PRIOR PELING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
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                                                                                                                                 Query Match 10.6%; Score 69.5; D
Best Local Similarity 25.0%; Pred. No. 0.58
Matches 30; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09193562D GENERAL INFORMATION:
                  TYPE: PRT; ORGANISM: Agrobacterium tumefaciens US-09-739-449-9534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                          67 KATLTVDISSSTAYM----
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US-09-193-562D-28
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Best Local Similarity
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LENGIH: 442
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Sequence 9534, Application US/09739449

GENERAL INFORMATION:
 APPLICANT: HINLE, Gregory J.
 APPLICANT: Slater, Steven C.
 TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(1549)0

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-3

NUMBER OF SEQ ID NOS: 13351

SEQ ID NO 9534
  RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 NYNQKFKGKATLTVDISSSTAY-MQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQPGAEL-VKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLE-WIGEIDPSESNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.0%; Score 105; DB 4; Length 128; 27.0%; Pred. No. 3e-05;
                                                                                                                                                                                                                                                         COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                          STREET: 1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23522-0157
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/475,815A FILING DATE: 07-JUN-1995
                                                                                                                          PILLSBURY WINTHROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030 REGERENCE/DOCKET NUMBER: 235 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
                                                          LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.0%
Best Local Similarity 27.0%
Matches 33; Conservative
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           TITLE OF INVENTION: RADI
TITLE OF INVENTION: LYMP
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                       CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-739-449-9534
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us-08-700-737-9.rapn

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Sequence 4, Application US/09814950
| GENERAL INFORMATION:
| APPLICATT WEI, MING-Hul et al. |
| TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOOL174
| CURRENT APPLICATION NUMBER: US/09/814,950
| CURRENT FILING DATE: 2001-03-23
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09814950
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01174
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTESO for Windows Version 4.0
                                                                                                                                                                  56 SNTNYNQKEKGKATLTVDISSSTAY-MQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQG 114
                                                                                                                                                                                          54 LRSGVPSRFSGS-----GSGTDYSLTINNLEPEDIATYFCQQ--YSRLPFT---FGSG 101
                                                                                         2 VQLQQPGAEL-VKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEID----PSE 55
                                                                                                                 3 QLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQ 62
                           Length 109;
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                                                           49; Indels
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                     9.5%; Score 62.5; DE
23.2%; Pred. No. 0.6;
Live 20; Mismatches
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9; Mismatches
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                 Query Match
Best Local Similarity 23.2%
Matches 29; Conservative
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Matches 20; Conservative
                                                                                                                                                                                                                                            115 TSVTV 119
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ORGANISM: Human
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US-09-814-950-2
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US-09-814-950-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HINKLE, Gragory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-223
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQL 83
                                                                                                                                                                                                    16;
                                                                                                                                                        DB 1; Length 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
                                                                                                                                                                                              33; Indels
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GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard
APPLICANT: Chen, Bl-Xing
TILE OF INVENTION:
TILE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JDW/SHS/MVM
CURRENT APPLICATION NUMBER: US/09/386,658
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%; Score 64; DB 5;
25.8%; Pred. No. 1.3;
ative 17; Mismatches 3:
                                                                                                                                                                                            15; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                    9.9%; Score 65; 24.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 SS----LTSEDSAVYYCA---RGGYDGWD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 ANAYUDLGTYGSITPYVGGGIGGSYVKWD 171
                                                                                                                                                                                                                                                                                                                                     113 SCSGTEQSVTECASRGWGNSDCTHD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-11638
                                                                                                                                                                                                                                                                                                  52 DPS---ESNTNYNOKFKGKATLTVD 73
                                                                                                                                                                  Similarity 24.79
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.88
Matches 23; Conservative
                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-739-449-11638
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: ORGANISM: mouse
US-09-386-658-4
                                                                                                                                               Query Match
Best Local Simi
Matches 21;
                                                                             ; ORGANISM: HOM
PCT-US01-09226-51
                                     753
                   SEQ ID NO 51
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29;

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36;

Length 172;

DB 5;

Score 62.5; DB Pred. No. 1; 9; Mismatches

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ch 9.5%; 1 Similarity 21.3%; 20; Conservative

Best Local Similarity Matches 20; Conserv

Query Match

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Search completed: April 13, 2001, 17:37:55 Job time: 171 sec
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         qq
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April 13, 2001, 17:35:03 ; Search time 117.03 Seconds (Without alignments) 166.311 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                        1 QVOLQOPGAELVKPGTSVKL.......DGWDYAIDYWGQGTSVTVSS 121
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Cgn2_6/ptodata/2/paa/US08_COMB.pep:*

Cgn2_6/ptodata/2/paa/US08_COMB.pep:*

Cgn2_6/ptodata/2/paa/US08_COMB.pep:*

Cgn2_6/ptodata/2/paa/US083_COMB.pep:*

Cgn2_6/ptodata/2/paa/US083_COMB.pep:*

Cgn2_6/ptodata/2/paa/US083_COMB.pep:*

Cgn2_6/ptodata/2/paa/US086_COMB.pep:*

Cgn2_6/ptodata/2/paa/US086_COMB.pep:*

Cgn2_6/ptodata/2/paa/US086_COMB.pep:*

Cgn2_6/ptodata/2/paa/US089_COMB.pep:*

Cgn2_6/ptodata/2/paa/US089_COMB.pep:*

Cgn2_6/ptodata/2/paa/US090_COMB.pep:*

Cgn2_6/ptodata/2/paa/US092_COMB.pep:*

Cgn2_6/ptodata/2/paa/US092_COMB.pep:*

Cgn2_6/ptodata/2/paa/US092_COMB.pep:*

Cgn2_6/ptodata/2/paa/US092_COMB.pep:*

Cgn2_6/ptodata/2/paa/US092_COMB.pep:*

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Cgn2_6/ptodata/2/paa/US096_COMB.pep:*

Cgn2_6/ptodata/2/paa/US096_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1009251 seqs, 160854530 residues
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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658
                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*
23: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 9, Appli Sequence 15, Appli Sequence 2, Appli Sequence 4, Appli Sequence 19, Appli Sequence 19, Appli Sequence 44, Appli Sequence 12, Appli Sequence 13, Appli Sequence 53, Appli Sequence 62, Appli
SUMMARIES	US-08-700-737-9 US-08-700-737-15 US-08-700-737-4 US-08-700-737-55 US-08-700-737-19 US-08-733-967-44 US-08-533-497-12 US-08-543-540-62
8 Ouery Match Length DB ID	121 140 1140 1144 1137 1137 1180 119 9 119 9 119 9
% Ouery Match L	100.0 100.0 100.0 98.2 86.9 86.9 81.5 79.8
Score	665 665 665 665 665 665 665 665 665 665
Result No.	12.642.01 01

•			Sequence 9, Appli									Sociones 72, Appl				sedneuce	ednence 6					Sequence 21 April	• •	• •	<b>5</b> u	ءَ ر	eduence o'	o apuanta	duence 34	ednence 7	edneuce 3	9	equence 11	1 -	onence 16	, ,	,	t annanha	
4 115-09-052-503	B 11S-09-408-646-	C 2 2 - 0 0 7 - 0 0 - 5 1 B	0-00-0	1 +00 100 00 00 0	1 03-08-1/9-184-	7 05-09-322-862-2	US-08-553-497-8	US-08-766-350-	1 US-08-766-350A-	2 US-08-836-455-48	5 US-09-120-809-7	7 US-09-313-928-3	7 115-09-313-928-	7 115-09-313-020-	7 115-09-312-030-	-076-CTC 60 CO V	-240-6	05-08-024-/12-6	US-08-443-540-6	US-07-881-109-2	US-07-881-109A-	US-08-31	1 US-08-720-323-	US-08-443-540-6	US-08-462-798-6	115-08-51	115-08-541	00-00	00-00-00	T-60-65	3 US-09-40	o US-09-159-027-	US-07-828-832-	US-08-465-473A-	US-07-828-832-1	US-08-465-473	115-08-443-540-14	•	
464	464	464	122	101	1 6	777	611	118																	119 8														
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# ALIGNMENTS

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US-08-700-737-9

Sequence 9, Application US/08700737

GENURAL INFORMATION:

APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Sedman, Jos
APPLICANT: Sedman, Jos
APPLICANT: Newman, HUMANIZED IMMUNOCLOBULIN REACTIVE MITH 4 7

ITILE OF INVENTION: INTEGRIN

UNMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Massachusetts
COUNTRY: USA
ZIP: 02173
COUNTRY: USA
ZIP: 02173
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REFERENCE/DOCKET NUMBER: LX895-10
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 121; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Lexington
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TOPOLOGY:
US-08-700-737-2
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                                                                                                                                                                                                                                                                          APPLICANT: Ponath, Paul D.
APPLICANT: Ponath, Paul D.
APPLICANT: Nones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Sendid, Mary M.
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             Length 121;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                           Score 658; DB 11;
Pred. No. 7.2e-58;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08700737 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTEREXSTICS:
LENGTH: 121 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATISH
                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                  Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-15
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                                                                                                                                ; TOPOLOGY: linear
US-08-700-737-9
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                61 NQKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSVIVS 120
                                                                                                                                                                                      Gaps
                                                                               1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKORPGQGLEWIGEIDPSESNTNY 60
                                                                                                       20 QVQLQOPGAELVKPGTSVKLSCKGYGYTFTSYWHHWVKQRPGQGLEWIGEIDPSESNTNY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: INTEGRIN
TITLE OF INVENTION: INTEGRIN
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Length 140;
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                                            Indels
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 658; DB 11;
100.0%; Pred. No. 8.8e-58;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  ; Score 658; DB 11;
; Pred. No. 8.6e-58;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: LA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,5
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: 121 amino acids
amino acid
                    Saldanha, Jos
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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US-08-700-737-55
                                                                                                                                                                                          COUNTRY:
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US-08-700-737-19
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80 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWQQGTSVTVS 139
                                                                                                                                 APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Singler, Douglas J.
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH 4 7
CORRESSONDENCES: 63
CORRESSONDENCES: 63
STRPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPQAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQELWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 137;
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/700,737 FILING DATE: 15-AUG-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
98.2%; Score 646; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;
Matches 118; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-640
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Ringler, Douglas J.
Jones, S. Tarran
Newman, Walter
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LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : MOLECULE TYPE: protein US-08-700-737-4
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APPLICANT:
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APPLICANT:
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61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWQQGTSVTVS 120
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Sequence 19, Application US/08700737

GENERAL INFORMATION:
APPLICANT: Bonath, Paul D.
APPLICANT: Stingler, Bouglas J.
APPLICANT: Application Walter
APPLICANT: Saldanha, Jos
APPLICANT: Allanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Massachnesee
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
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                                                                                                                                                                                                                                                ; DB 11;
2.6e-49;
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86.0%; Pred. No. 2.6e-
iive 7; Mismatches
                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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61 NQKFKGKATLITVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFRRATLIYODKSSSTVYMQLSSLTSEDSAVYYCARSG--GFYYGMDYWGGGTSVTVS 118
                                                                                                                                                                                                                                                                                                                       1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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TITLE OF INVENTION: Anti-EGFR Single-Chain Fvs and Anti-EGFR
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119;
                                                                                                                                                                                                                                                  Length 119;
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85.1%; Pred. No. 9.7e-46;
tive 4; Mismatches 12.
                                                                                                                                                                                                                                                    81.5%; Score 536; DB 4;
84.3%; Pred. No. 9.7e-46;
iive 5; Mismatches 12
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/050001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497
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US-08-553-497-12
Sequence 12, Application US/08553497
GENERAL INFORMATION:
             REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 12:
                                                                                                           44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 103; Conservative
                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                              Query Match
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                                                             MCDUDING TIPE FIRM PG COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PACENTIN Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: BTOOK, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 861-6240
TELEFAX: (617) 861-6540

TELEFAX: (617) 861-6540

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Syamal K. Datta
TITLE OF INVENTION: METHODS FOR INHIBITING THE
TITLE OF INVENTION: ACTIVITY OF PATHOGENIC T
TITLE OF INVENTION: HELPER CELLS ASSOCIATED WITH
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TYPE: 3.5" Diskette, 1.44 Mb Mb Mb TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: IBM P.C. DOS (Version 3.30) SOFTWARE: WordPerfect (Version 5.0) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/073,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 572; DB 11;
Pred. No. 4.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/764,686
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/08073967
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.9%;
86.0%;
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TYPE: amino acid
TOPLOGY: 1:
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                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.0
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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             ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02110-2804
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GENERAL THOURANTION:
GENERAL THOURANTION:
GENERAL THOURANTION:
APPLICANT: Obtaunt, Jun
APPLICANT: Obtaunt, Jun
APPLICANT: Obtaunt, Jun
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Yoshida, Hiroko
APPLICANT: Yoshida, Hiroko
APPLICANT: Yoshida, Akio
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126/HG
CURRENT APPLICATION NUMBER: US/09/053,583A
CURRENT APPLICATION NUMBER: JP HEI 9-82953
EARLIER APPLICATION NUMBER: JP HEI 9-16908
EARLIER FILING DATE: 1997-06-25
EARLIER APPLICATION NUMBER: JP HEI 9-276664
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
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Best Local Similarity 83.7
Matches 103; Conservative
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STRANDEDNESS: sir
                                                            Y: USA
94304-1018
                      Palo Alto
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US-08-443-540-62
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                                                              COUNTRY:
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                                                                                                APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Sunder, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HURBGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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Pred. No. 1.3e-44;
1; Mismatches 16; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Application US/08443540
Sequence 62, Application US/08443540
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1996
15-AUG-1996
18-AUG-1996
18-AUG-1996
                                                              Sequence 53, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVIG
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 79.5%;
Slmilarity 79.5%;
01; Conservative
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                               CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||||
| 121 TTVTVSS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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US-08-700-737-53
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Best Local Simi
Matches 101;
                    RESULT 9
US-08-700-737-53
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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61 NOKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%; Score 524; DB 8; Length 119
83.7%; Pred. No. 1.5e-44;
tive 5; Mismatches 9; Indels
                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 105/08/443,540
FILING DATE: 105/08/443,540
FILING DATE: 105/08/443,540
FILING DATE: 105/08/443,540
ATTORNEY/AGENT INFORMATION:
NAME: KOSIKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEENA: (415) 813-5600
TELEEX: 706141 CIOTTI UD
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/09053583A; GENERAL INFORMATION:
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MOLECULE TYPE:
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                                                                                                                                                                     Gaps
                                                                                                                                                                                                    1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGGELEWIGEIDPSDSSYTNY 79
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                                                                                                                             Length 464;
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                                                                                                                                                                   Indels
                                                                                                                             79.5%; Score 523; DB 14;
83.5%; Pred. No. 9.5e-44;
                                                                                                                                                  Pred. No. 9.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/408,646A CURRENT FILING DATE: 1999-09-30 BARLIER APPLICATION NUMBER: JP 10-276881 EARLIER FILING DATE: 1998-09-30 NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-408-646-9
Sequence 9 Application US/09408646A
SEQUENCE 9 Application US/09408646A
GENERAL INFORMATION:
APPLICANT: Barizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTION: ANTIF Fas Antibodies
FILE REFERENCE: 990540/HG
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US-09-409-662-9
IS-09-409-662-9
SEQUENCE 9 Application US/09499662
GENERAL INFORMATION:
APPLICANT: SCTIZAWA, NODUÍUSA
APPLICANT: HATUYAMA, HIGGYUKI
APPLICANT: NARABARA, KAOFÍ
APPLICANT: TAMARÍ, IKUKO
                                                                                                                                              Best Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Takahashi, Tohru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                    ) ORGANISM: Mus musculus US-09-053-583-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-408-646-9
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Matches 101; Conserv
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                   LENGTH: 464
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SEQ ID NO 9
                                    TYPE: PRT
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Sequence 28, Application US/08692084
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MON
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                             Length 464;
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,084
FILING DATE: 08-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/236,520
APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             Score 523; DB 18;
Pred. No. 9.5e-44;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1199-1-001 CIP
                        FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/09/499,662
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: US 09/053,583
EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ 1D NOS: 165
SEQ 1D NO 9
TITLE OF INVENTION: Anti-Fas Antibodies FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                             Query Match 79.5%;
Best Local Similarity 83.5%;
Matches 101; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus US-09-499-662-9
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Best Local Similarity
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protein

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Search completed: April 13, 2001, 17:37:47 Job time: 164 sec
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                                                                                                                                                     1 QVQLQQPCAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rodriguez, Moses
APPLICANT: Milet, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
CORRESPONDENCE ADDRESS:
                                                            Score 520.5; DB 10; Length 122;
Pred. No. 3.5e-44;
4; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
FILING DATE: 07-JAN-1997
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US/08/52,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEGOMMULCATION NUMBER: 201-487-5800
TELEGOMMULCATION NUMBER: 201-487-5800
TELEGOMMULCATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 Anhno acids
TYPE: Annho acids
TYPE: Annho acids
TYPE: ANNHO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-779-784-28; Sequence 28, Application US/08779784; GENERAL INFORMATION:
                                                               79.1%;
81.1%;
                                                          Query Match
Best Local Similarity 81.18
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-779-784-28
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US-08-692-084-28
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Gaps

Query Match

79.1%; Score 520.5; DB 11; Length 122;
Best Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1;

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1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                 SS 121
                                                                  SS 122
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Appl Appl

Seguence Sequence Seq

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GENERAL INFORMATION:
APPLICANT: RETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: BENDIG, MARY M.
APPLICANT: ADAN: JAUME
APPLICANT: ADAN: JAUME
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: BLASCO, FRANCESC
APPLICANT: BLASCO, FRANCESC
APPLICANT: NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEF: MITLE OF INVENTION: ANTIEDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
COUNTRY: US
COUNTRY: US
SIP: 22201
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIA PC-DOS/MS-DOS
SOFTWARE: PACEDIATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLEASIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: E 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: E 94118970.6
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INPOMMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION UNMBER: B 94118970.6
FILING DATE: 0.2-DEC-1994
ATTORNEY/AGENT INPOMMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION UNMBER: 33,302
US-08-894-922A-14
US-08-894-922A-14
US-08-881-037-16
US-09-065-059-5
US-08-737-56A-10
PCT-US91-11611-4
US-08-553-497A-22
US-08-658-57
US-08-469-468-57
US-08-811-037-17
US-08-811-037-17
US-08-811-037-15
US-08-811-037-15
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08553497A
Patent No. 5844093
                                                       TELEPHONE: 703-243-633
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
  RESULT 1
US-08-553-497A-12
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                                                                                                                                                         April 13, 2001, 15:34:02; Search time 28.17 Seconds (without alignments) 82.517 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         US-08-700-737-9
658
1 QVQLQQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVIVSS 121
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Sequence
Sequence
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(Ggn2_6/ptodata/2/laa/5A_COMB.pep:*

(Cgn2_6/ptodata/2/laa/5B_COMB.pep:*

(Ggn2_6/ptodata/2/laa/5A_COMB.pep:*

(Ggn2_6/ptodata/2/laa/6A_COMB.pep:*

(Ggn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

(Ggn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-553-497A-12

US-08-81-037-62

US-08-81-037-62

US-08-557-497A-8

US-08-553-497A-8

US-08-353-400-35

US-08-353-400-35

US-08-421-988-3

US-08-421-988-7

US-08-491-988-7

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US-08-491-988-7

US-08-491-988-7

US-08-881-037-61

US-08-881-124

US-08-881-11

US-08-455-473B-11

US-08-455-473B-11

US-08-455-473B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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US-08-553-497A-24
US-08-737-560A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185757 seqs, 19210857 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                         Title:
Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                    Sedneuce:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                            Run on:
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61 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYAIDYWGQGTSVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 122;
                                                                                                                                                                                                                                                                                                                      APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
9; Indels
                                                                                                                                                                                                                                                                                                                                                        STEET: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
UDITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.1%; Score 520.5; DB 1;
81.1%; Pred. No. 9e-41;
Live 4; Mismatches 18;
 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MMV92-01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 9, Application US/08236520; Patent No. 5591629; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...: $
...rebistics:
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.... 122 amino acids
TYPE: amino acid
TOPOLOGY: 1:-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-236-520-9
      Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 99; Conserv
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US-08-236-520-9
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                                                                                                                                          Length 119;
                                                                                                                                            81.5%; Score 536; DB 2; Length 11
ilarity 85.1%; Pred. No. 3.4e-42;
Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NATA: TLING DATE: VS/08/081,037 FILING DATE: VS.2UN-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 524; DB 3;
Pred. No. 4.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Application US/08881037
Patent No. 6080588
GENERAL INPORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203442110710
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APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
GLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
WIDTOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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83.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 494-0792
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                  SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
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                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-12
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Best Local Similarity
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ZIP: 94304-1018
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                                                                                                                                                               Best_Local Similarity
Matches 103; Conserv
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61 NOKFKGKATLÍVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.0%; Score 520; DB 2; Length 119; Best Local Similarity 81.8%; Pred. No. 9.8e-41; Matches 99; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
CLLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/0097B
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 10-MAR-1995
FILING DATE: 17-MAR-1994
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 17-MAR-1994
APPLICATION NUMBER: BP 94118970.6
FILING DATE: NOWBER: BP 94118970.6
                                                                                                                                                 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 CLTY: ARLINGTON STATE: VA COUNTRY: US
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APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTIEGD
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
        BLASCO, FRANCESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                      APPLICANT: Mayo Foundation for Medical Education Research TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION CORRESPONDENCE: 11
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTY: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: APril 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Pattila,
REGISTRATION NUMBER: 27,227
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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                                                     Sequence 9, Application PC/TUS9505262 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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MITJANS, FRANSESC
ROSELL, ELISABET
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ANSELL, KEITH H.
GUSSOW, DETLEF
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  CITY: Lexington
STATE: Massachusetts
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APPLICANT: KETTLEBO
APPLICANT: BENDIG,
APPLICANT: GUSSOW,
APPLICANT: ADAN, JA
APPLICANT: MITJANS,
APPLICANT: ROSELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
          RESULT 4
PCT-US95-05262-9
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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        RESULT
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Query Match
Best Local Similarity
Matches 97; Conserv
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US-08-491-988-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 520; DB 1; Length 445; 80.2%; Pred. No. 4.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILLIG DATE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DAYE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SI, OUENCES: 37
COMPUTER RELABLE FORM:
MEDIUM TYIE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATT: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9411089.7
FILING DATS: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 33:
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LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-353-400-36
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYP3: protein US-08-353-400-33
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Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                         20 QVQLQQPGAELVKPGASVQLSCKASGYTFTGYWIHWVKQRPGGCLEWIGEVNPSTGRSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 269;
79.0%; Score 520; DB 1; Length 464; 80.2%; Pred. No. 4.5e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 517.5; DB 2
Pred. No. 4.1e-40;
4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
CORRESPONDENCE: 80
CORRESPONDENCE ADDRESS:
                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/428,257A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  Sequence 72, Application US/08428257A Patent No. 5885808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS:
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 269 amino acids
amino acid
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Best Local Similarity 81.89
Matches 99; Conservative
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                                          97; Conservative
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10016-2391
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 261 Ma
CITY: New York
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 517.5; DB 2; Length Pred. No. 6.5e-40; 4; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible COMPUTER: 1BM PC COMPATIBLE COMPATION STREET: PATENTIA NECTORS/MS-1:0, Version #1.25 CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/491,988 FILING DATE: 18-DEC-1995 CLASSIFICATION: 424 ATONINYARINIA INFORMATION: NAME: GOLDBERG, JULES E. REGISTRATION NUMBER: 24,408
                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEDNARALN, MAHENDRA
APPLICANT: DEDNARALN, MAHENDRA
NUMBER OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                           APPLICATION NUMBER: US/08/491, CLASSIFICATION NUMBER: US/08/491, CLASSIFICATION: 424 ATTORREYAGENT INFORMATION: NAME: COLDBERG, ULLES E. RELECOMMUNICATION NUMBER: 24,408 TELEFONE: 212-986-4090 TELEFAX: 212-986-4090 TELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08491988
Patent No. 5973116
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
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81.8%;
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amino acid
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Best Local Similarity 81.8
Matches 99; Conservative
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INFORMATION FOR SEQ ID NO:
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LENGTH: 415 amino aci
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; MOLECULE TYPE: protein
US-08-491-988-9
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ZIP: 10016-2391
COMPUTER READABLE FORM:
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US-08-491-988-7
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STREET: 261 MADISON AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                           ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
STREET: NEW YORK
STATE: NY
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: IB-DEC-1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.6%; Score 517.5; DB 2; 81.8%; Pred. No. 4.1e-40;
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APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEDNARANI, MAHENDRA
ATTLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                    APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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Sequence 9, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-491-988-3
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APPLICANT:
                                          APPLICANT:
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61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYCAKGRLRY----FAMDYWGQGTSVT 116
61 NQKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                Sequence 61, Application US/08881037 Patent No. 6080588
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TELEFAX: (650) 494-0792
TELEX:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-08-881-037-63
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                                                                                                                                                                                                                                                        61 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                       Gaps
                                                                                                                                                                       1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                      23 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 82
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                                                                                                                                      1;
                                                                                                      Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 517.5; DB 2;
Pred. No. 7.1e-40;
4; Mismatches 17;
                                                                                                    Score 517.5; DB 2
Pred. No. 6.7e-40;
4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: CEONARAIN, MAHENDRA
TITLE OF INVEWIION: Compounds for targeting
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: GOLCBERG, JULES E.
REGISTRATICN NUMBER: 24,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 212-986-4090 TELEFAX: 212-818-9479
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81.8%;
                                                                                                    78.6%;
81.8%;
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amino acid
                                                                                               Query Match
Best Local Similarity 81.84
Matches 99; Conservative
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Best Local Similarity 81.8 Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-491-988-5
                             MOLECULE TYPE: protein US-08-491-988-7
     amino acid
                    linear
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                    TOPOLOGY:
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US-08-491-988-5
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Search completed: April 13, 2001, 15:36:09 Job time: 127 sec
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Pred. No. 2.3e-40;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                               COUNTY: USA

ZIP: 94304-1018

COUNTY: USA

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible .

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

CLASSIFICATION: 530

PRICK APPLICATION DATA:

APPLICATION NUMBER: US 08/443,540

FILING DATE: 18 MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, Antoinette F.

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 33,202

REGISTRATION NUMBER: 33,202

REGISTRATION NUMBER: 33,202

REGISTRATION NUMBER: 203442110710

TELECOMMUNICATION INFORMATION:

TELEFHONE: (650) 813-5600

TELEFAX: (650) 494-0792
Sequence 63, Application US/08881037
Fatent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOEISTER
STREET: 755 Page Mill Road
CTITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-00-881-037-60

Sequence 60, Application US/08881037

Sequence 60, Application US/08881037

GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 82.1%;
Matches 101; Conservative
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61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 513; DB 3; Length 11
Pred. No. 4.2e-40;
8; Mismatches 9; Indels.
                                     COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.0%;
Best Local Similarity 81.3%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
COUNTRY: USA
ZIP: 94304-1018
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein . protein search, using sw model

April 13, 2001, 15:36:46 ; Search time 32.39 Seconds (without alignments) 280.069 Million cell updates/sec Run on:

US-08-700-737-12 695 1 MKLPVRLLVLLLFWIPVSGG.......CLQGTHQPYTFGGGTKLEIK 132 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

198801 seqs, 68722935 residues Searched:

198801 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_67:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	31	32	33	34	35	36	37	38	39	40	41	42	6		44	45

# ALIGNMENTS

RESULT

B25912 ,	Ig kappa chain precursor V region (W3129) - mouse (fragment)	C; Species: Mus musculus (house mouse)	C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text change 21-Jan-2000	C; Accession: B25912	R;Borden, P.; Kabat, E.A.	Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443. 1987	A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light	A; Reference number: A94147; MUID:87175689	A; Accession: B25912	A; Molecule type: mRNA	A; Residues: 1-132 <bor></bor>	A:Cross-references: GB:M15874; NID:q196839; PIDN:AAA38796 1; PID:q196840	A; Note: the authors translated the codon CTC for residue 100 as car	C; Superfamily: immunoglobulin V region: immunoglobulin homology	C; Keywords: heterotetramer; immunoglobulin	F:1-19/Domain: signal sequence (fragment) #status predicted <816>	F;20-132/Product: Iq kappa chain V region W3129 #sfatus predicted cvap.	F:35-114/Domaio imminoral challes bomed care crass	
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Gaps ö Query Match

89.2%; Score 620; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 2.3e-47;
Matches 118; Conservative 4; Mismatches 8; Indels

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123 FGGGTKLEIK 132 οy

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RESULT H30560

Types chain V region (36.1.2D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 3.3 Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000
C;Accession: H30560
R;Matsuda, T.; Rabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Titje: Variable region cDNA sequences and antigen binding specificity of mouse mono

A;Reference number: A30560; MUID:89110062 A;Accession: H30560 A;Status: preliminary

Length 112,

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Score 553.5;
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                          81.0%;
94.6%;
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Best Local Similarity
Matches 106; Conserv
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                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                            Query Match
                                                  Local
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                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig kappa chain V region (16.4.12E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mar musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
C;Accession: 830540
R;Matsuda, T : Kahat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monocle
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
Cispate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
Ciscession: S37203
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. submitted to the EmBL Data Library, August 1993
A;Description: Production and cloning of TWV-specific monoclonal antibodies.
A;Reference number: S37200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference numbe:: A30560; MUID:89110062
A;Accession: E305:0
A;Status: preliminary
A;Molecule type: nRNA
A;Residues: 1-113 < MAT>
A;Cross-reference:: GB:M24272; NID:9197079; PIDN:AAA63369.1; PID:9197080
A;Cross-reference:: GB:m24272; NID:9197079; PIDN:AAA63369.1; PID:9197080
A;Note: the autho:: translated the codon GTA for residue 30 as His
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: inmunoglobulin homology <IMM>
A; Wolecule type: mRNA
Asesidues: 1-113 <AMAT>
A; Residues: 1-113 <AMAT>
A; Cross.references: GB:M24275; NID:g197085; PIDN:AAA63372.1; PID:g197086
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterctetramer: immunoglobulin homology
F; 16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                  SGVPDRF&GSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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                                                                                                                                                           Score 576; DB 2; Length 11 Pred. No. 1.3e-43; 0; Mismatches 3; Indels
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Pred. No. 2e-43;
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Best Local Similarity 97.3%;
Matches 109; Conservative
                                                                                                                                                           Query Match 82.9%;
Best Local Similarity 97.3%;
Matches 109; Conservative (
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A;Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:q639656; PIDN:AAA61589.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A,Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis
A,Reference number: A39276; MUID:91088540
A,Recession: B39276
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                                                                                                                                                                                                                                                                                                                                                                                                                        Ig light chain precursor V-D-J region (6-19) - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000 C;Accession: B39276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Modecule type: mRNA
A; Modecule type: mRNA
A; Residues: 1-131 < REL>
A; Cross-references: GB:M55313; NID:9198095; PIDN:AAA63385.1; PID:9198096
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 35-114/Domain: immunoglobulin homology < IMM>
                                                                                                                   DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF
                                                                                                                                                  ä
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                                                                                                                                                                                                                                                             Length 131;
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A; Title: Active site structure and antigen binding properties of A; Reference number: A34903; MUID:90094387
A; Accession: B34904
A; Status: preliminary; not compared with conceptual translation
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                                                                     Indels
, DB 2; ....
. 1.8e-42;
3;
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80.3%; Pred. No. 3.5e-42;
live 10; Mismatches 15
                                                                       Mismatches
              Score 563;
Pred. No. 1.
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Length 131;

DB 2;

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Query Match 78.9%
Best Local Similarity 94.7%
Matches 107; Conservative
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A; Status: preliminary; not compared with conceptual translation
A; Molecule type; manA
A; Molecule type; manA
A; Molecule type; manA
A; Residues: 1-131 < BED>
R: BedZyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
A; Residues: 1-131 < BED>
A; Tiol. Chem. 264, 1565-1569, 1989
A; Title: Comparison of variable region primary structures within an anti-fluorescein idi
A; Reference number: A31485; MUID: 89109167
A; Recession: 131485
A; Accession: 131485
A; Residues: 20-52 < EB2>
A; Residues: 20-52 < EB2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 35-114/Domain: immunoglobulin homology < TMM>
                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V region (3-24) - mouse (5.5pecies: Mus musculus (house mouse) (5.5pecies: Mus musculus (house mouse) (5.5pecies: 27-3ul-1990 #sequence_revision 27-3ul-1990 #text_change 21-Jan-2000 (5.Accession: C34904: 131485 ** Redayk, W.D.: Herron, J.N.: Edmundson, A.B.: Voss Jr., E.W. A: Bidol. Chem. 265, 133-138, 1990 ** A:Title: Active site structure and antigen binding properties of idlotypically cross-real A:Reference number: A34903; MUID:90094387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arti-DNA autoantibody BV16-13, kappa chain V region - mouse (fragment)
(Species: Mus musculus (house mouse)
(Species: Was musculus (house mouse)
(Space: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
(SACcession: PL0202
R:Smith, R:G:, Voss Jr., E.W.
MOL. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from A:Reference number: PL0198; MUID:90309768
A:Accession: PL0202
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                                                                                    1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
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      1.4e-41;
thes 16;
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Pred. No. 3.2e-41;
); Mismatches 17
    ed. No. 1.46
Mismatches
      Pred.
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79.5%; Pred
9; V
  80.3%;
                     106; Conservative
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-114 <SMI>
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Best Local
Matches 10
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C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 21-Jan-2000
C;Accession: B30577
R;Kofler, R; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A;Accession: B30577; MuID:85159423
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A;Cross-references: GB:X53642; NID:950192; PIDN:CAA37693.1; PID:9930138 C.Superfamily: immunoglobulin V region; immunoglobulin homology cIMM> F:26-95/Domain: immunoglobulin homology cIMM> F:24-39/Region: complementarity-determining 1 F;55-67/Region: complementarity-determining 2 F;55-67/Region: complementarity-determining 2 F;9102-114/Region: Complementarity-determining 3 F;102-114/Region: JH region
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A;Residues: 1-131 <KOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 548.5; DB 2
Pred, No. 3.4e-41;
1; Mismatches 4
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Pred. No. 5.9e-41;
8; Mismatches 18
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94.7%;
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Best Local Similarity 79.5%;
Matches 105; Conservative
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F;35-114/Domain: immunoglobulin homology <IMM>

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Ig Kappa chain V region (38C13.V7) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C; Accession: PS0074
R; Levy, S.; Campbell, M.J.; Levy, R.
J. Expy Med. 170, 1-13, 1989
J. Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrang A; Reference number: A92781; MUID:89310348
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C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 263, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for t
A;Reference number: A25612; MuID:88007582
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                                                                               Length 132;
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Pred. No. 2.6e-40;
3; Mismatches 18; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-131 <CHE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin C; Keywords: heteroterramer; immunoglobulin F;34-113/Domain: immunoglobulin homology <IMM>
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                                                                                   Score 540.5; DB Pred. No. 2e-40;
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ilarity 79.5%;
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A; Status: translation not shown
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R;Bedzyk, W.D.; Hirron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
R;Bedzyk, W.D.; Hirron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
A;Title: Active s:te structure and antigen binding properties of idiotypically cross-rea A;Reference numbe.: A34903; MUID:90094387
A;Reference numbe.: A34904
A;Recession: D349:04
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-131 < RED>
A;Residu
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A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain A;Reference number: PH0105; MUID:91015092
A;Accession: PH0106
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C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C;Accession: PH0106
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C;Species: Mus mu:culus (house mouse)
C;Date: 27-Jul-19:0 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
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A;Molecule type: nRNA
A;Residues: 1-132 <NRA
C;Superfamily; immunoglobulin V region; immunoglobulin homology
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Pred, No. 5.9e-41;
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C; Keywords: heterctetramer; immunoglobulin F;35-114/Domain: immunoglobulin homology <IMM>
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Ribedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-rea
A;Reference number: A34903; MUD:90094387
A;Accession: G34903

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C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
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US-08-700-737-12 695 1 MKLPVRLLVLLEWIPVSGG.......CLQGTHQPYTFGGGTKLEIK 132 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

93435 Total number of hits satisfying chosen parameters: 93435 segs, 34255486 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NON_TER
SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; detazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eitheria; Primates; Catarrhini; Hominidae; Homo.
NCbI_TaxID=1606;
                                                                                                                                                                                                                                                                                           Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eu:heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=1)090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.8%; Score 471; DB 1; Length 113; 80.4%; Pred. No. 2.9e-40; ive 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORN 1.
COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region; Monoclonal antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.7AN-1988 (Rel. 06, Created)
01.7AN-1988 (Rel. 06, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
16.G KAPPA CHIN V-II REGION GM607 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                           21-JUL-1986 [Rel. 01, Created)
21-JUL-1986 [Rel. 01, Last sequence update)
15-JUL-1999 [Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 26-10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                STANDARD;
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                                                          121 YTFGGGTHLEIK 132
                                                                              :||| || :|||
121 WTFGQGT!:VEIK 132
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA;
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SEQUENCE FROM N.A.
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01-JAN-1988 (
15-JUL-1999 (
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Best Local Simi
Matches 90;
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P06309;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A/J;
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SEQUENCE
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KV2G_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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MEDLINE=74148480; PubMed-4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.",
Biochemistry 12:3763-3780(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F., Glenner G.G.; "Structural identity of Bence Jones and amyloid fibril proteins in patient with plasma cell dyscrasia and amyloidosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SSGDIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 NRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-II REGION GM607. FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING
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COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 422; DB 1;
Pred. No. 2.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-IT REGION TEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AA
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                                                                                                                                                                                                                                                                                                                                   EMBL; Z00009; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; -.
Pfam; PF00047; ig; 1
Immunoglobulin V region; Signal.
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llarity 71.3%;
Conservative 1:
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27
43
58
65
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116
                                                                                                Nature 309:73-76(1984)
                                                                                                                                                                                                                                                                                                                                                              PIR; A01889; K2HUGM
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P01617;
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Similarity 72.69
82; Conservative
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                                                                                                                                              KV2B_HUMAN
P01615;
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P18135;
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          Best Local
Matches 8
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       "INSCELLANEOUS: THE MAJOR ANYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

"INSCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.

"INSCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                               21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
"I- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
"I- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01885; K2HUCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                               Length 113;
                                                                                                                                                           COMPLEMENTARITY - DETERMINING
                                                                                                                                       COMPLEMENTARITY - DETERMINING FRAMEWORK 3.
                                                                                                                                                                                                                                                 19; Indels
                                                                                                   protein; Amyloid.
                                                                                                                                                                                               0C3C38F81F1843CA CRC64;
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                                                                                                                                                                                                                            ; Score 418; DB 1;
; Pred. No. 5.4e-35;
15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
IG KAPPA CHAIN V-II RECION CUM.
HOMO SAPLENS (Human).
RECION ABORDA (Human).
MARATYOLA MELAZOA: Chordata; Craniata; Vertel Mammalla; Eutherta; Primates; Catarrhini; Homi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR003006; -
Pfam: PF00047: 1g; 1
Immunoglobulin V region; Bence-Jones protein.
                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                             115 AA
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                                                                                                            FRAMEWORK
                                                                                                                                FRAMEWORK
                                                                PIR; A01888; K2HUTW.
InterPro; IPR003006; --
Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Bence-Jones
 Clin. Invest. 52:1276-1281(1973)
                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MEDLINE=70063440; Pubmed=4188189;
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                                                                                                                                                                                              12316 MW;
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69.6%;
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102
112
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                                                                                                                                                                                             113 AA;
                                                                                                                                                                                                                                   Local Similarity
les 78; Conserv
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103
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21-JUL-1986
                                                          MARKER
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P01614;
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SEQUENCE
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KV2A_HUMAN
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Gaps
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                                                                            MEDLINE-76253627; Pubwed-821524;
Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms Igm
"Variable region sequence of the bloth chain from a Waldenstroms Igm
with specificity for phosphorylcholine.";
Biochemistry 15:3829-3831(1976).
-! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  80 FSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
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72.6%; Pred. No. 7.8e-35;
tive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION FR.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-III REGION HAH PRECURSOR.
                                                                                                                                                                                                                                                                           113 AA
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                                                                                                                                                                                                                                                                         STANDARD;
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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39
54
61
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112
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Length 115;

DB 1;

59.9%; Score 416.5;

Query Match

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4; Gaps

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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                      1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-III REGION HIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING 1.
                                                            FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                       57.6%; Score 400; DB 1; Length 129; 56.1%; Pred. No. 3.9e-33; ive 28; Mismatches 26; Indels
                                                                                                             FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
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                                                                                              COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                     14070 MW; 7395528EA2BB74D6 CRC64;
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65.2%; Pred. No. 9.3e-33;
Live 20; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1996 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION MIL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA
                                                                                                                                     JK1 SEGMENT.
BY SIMILARITY.
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                          region; Signal.
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38
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InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region;
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                                                                                                                                                                                                                                                                                                                                                                                    117 WIFGOGTKVEIK 128
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Best Local Similarity
Matches 74; Conserv
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129 #
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21-JUL-1986
15-JUL-1999
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Best Local Simi
Matches 73,
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P01616;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                      Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).

-i- DISEARS: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUTOANTIEODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              IG KAPPA CHAIN V-III REGION HAH.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                          Length 129;
                                                                                                                                                                                                                                                                                            FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                   26; Indels
                                                                                                                                                                                                                                                                                                                                               129
14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          57.7%; Score 401; DB 1;
56.8%; Pred. No. 3.1e-33;
ive 27; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHLIN V-III REGION HIC PRECURSOR.
EUKAPYOTA: (Human).
EUKAYOTA: (Hetazoa: Chordata: Craniata; Vertek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AA.
                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
                                    SEQUENCE FROM N.A. MEDLINE=88171307; PubMed=3127527;
                                                                                                                                                                                                           region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
                                                                                                                                                                   InterPro; IPH:003006; -. Pfam; PF0004; ig; 1. Immunoglobul.n V region: SIGNA.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 RIFGOGIKVEIK 128
                                                                                                                                                            PIR; PL0022; K3HUHA.
HSSP; P01789; 2MCP.
                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID="606;
             NCBI_TaxID=9606;
                                                                                                                                                   LEUKEMIA.
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P18136;
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Length 112;

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MEDLINE-83256427; pubmed-6409088; Chang J.Y., Herbst H., Aebersold R., Braun D.G.; Chang J.Y., Herbst H., Aebersold R., Braun D.G.; A new isotype sequence (V kappa 27) of the variable region of kappa-light Chains from a mouse hybridoma-derived anti-(streptococcal group A polysaccharide) antibody containing an additional cysteine residue. Application of the dimethylaminoacobenzene isothiocyanate technique for the isolation of peptides."; Biochem. J. 211:173-180(1983).

-!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ambersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
"Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
origin: monoclonal antibodies 17829.1 and 22825.1 specific for the
agroup A-streptococcal polyancharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
-!-MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
InterPro; IPR003006;
Pfam; PF00047; 19:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                            FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                               Immunoglobulin V region; Monoclonal antibody; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                   12496 MW; 42C019D10ADA3C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 394; DB 1;
Pred. No. 1.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 17S29.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                               56.7%;
67.9%;
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Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                 InterPro; IPR003006; -. Pfam; PF00047; 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                 113 AA;
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P03976;
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
            DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                     61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCANLQELPYTFGGGTKLEIK 112
                                                                     SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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S6.8%; Score 395; DB 1; Length 112;
Best Local Similarity 67.9%; Pred. No. 1e-32;
Matches 76; Conservative 11; Mismatches 25; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 251.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin V region; Monoclonal antibody.
DOMAIN 1 23 FRAMEWORK 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 7S34.1.
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P01630;
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KV4C_HUMAN
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MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mous: kappa variable regions.";
Proc. Natl. icad. Sci. U.S.A. 75:3913-3917(1978).
PIR: A01995; KVMSM6.
InterPro; IPH003006; -
Pfam: PF0004"; ig; 1.
                                                                        Gaps
                                                                                           21 DVVVTQTFLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                     Burstein Y., Schechter I.; "Primary strictures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: .mplications on the organization and controlled expression of immunoglobulin genes.";
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=1(.090;
                                                                                                                                                                                                                                                                                                                                                                                                                                       McKean D.J., Potter M., Hood L.E.;
Mouse immunicaboulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-III REGION MOPC 63.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
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                                                                                                                                   SGVPDRF: GSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                              Length 113;
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                                                  56.4%; Score 392; DB 1; Length 11 67.0%; Pred. No. 2.1e-32; ive 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING
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                      4E93797046F8DB33 CRC64;
                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
                                                                                                                                                                                                          131 AA
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   BY SIMILARITY.
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BY SIMILARI
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MEDLINE=7823:887; PubMed=98179;
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                      MM;
                      12390
                                                    Query Match 56.49
Best Local Similarity 67.09
Matches 75; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
  23
113
113 AA;
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P01661;
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Score 387.5; DB 1; Length 131; Pred. No. 7e-32;

55.8%; 56.8%;

Query Match Best Local Similarity

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                                                                                          61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                        Gaps
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                          1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

BEDLINE-86041854; PubMed=2997713;
MATSh P., Mills F., Gould H.;

"Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14966 MW; 6413A22FD0738832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                           134 AA.
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Nucleic Acids Res. 13:6531-6544(1985)
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01-APR-1988 (Rel. 07, Last seq
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Best Local Similarity
Matches 76; Conserv
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REVISION TO 76.
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P06314;
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                              60 WYLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQCTHQ 119
                                                61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAYYCQQYYNL 120
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FRAMEWORK 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
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                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
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Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                          STANDARD;
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121 PWTFGQGTKVEIK 133
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P06311;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

April 13, 2001, 15:39:52 ; Search time 56.51 Seconds (without alignments) 273.782 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 seqs, 117207915 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL\_15:\* Database :

sp\_archea:\* sp\_bacteria:\*

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_rodent:\* sp\_unclassified:\* sp\_vertebrate:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* sp\_virus:\* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

091182 mus musculu Q9ul80 homo sapien Q9ul78 homo sapien Q9ul77 homo sapien Q9ul77 homo sapien Q9ul70 homo sapien Q91170 homo sapien Q91170 homo sapien Q9118 homo sapien Q9118 homo sapien Q9118 homo sapien Q9118 mus musculu Q9ul83 homo sapien Q9118 mus musculu Q9118 mus musculu Q9118 mus musculu Q91176 mus musculu Q910005 oryctolagus Description SUMMARIES Q9JL82 Q9UL80 Q9UL71 Q9UL77 Q9UL70 Q9UL70 Q9UL70 Q9UL85 Q9UL85 Q9UL83 Q9UL81 Q9 Query Match Length DB Score 447 412.5 334.5 326.5 326.5 326.5 319.5 319.5 319.5 319.5 311.5 311.5 311.5 249.5 249.5

Ognsd6 homo sapien Ognp29 homo sapien Ogu182 homo sapien Ogu182 homo sapien Og8907 mus musculu Og8907 mus musculu Ogu456 homo sapien Ogu455 homo sapien Ogu455 homo sapien Ogu455 homo sapien Ogu456 homo sapien Ogu456 homo sapien Ogu4513 homo sapien Ogu413 homo sapien Ogu4189 homo sapien Ogw8m7 salmiri sci Ogy8m7 salmiri sci Ogsm7 kmgculu Og5776 homo sapien	Q9xsm6 saimiri sci Q94vV0 homo sapien Q91bO2 sphoeroides Q08835 cercopithec Q91bO5 sphoeroides O46632 bos taurus
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1130 1030 1030 1040 1050 1050 1050 1050 1050 1050 105	235 397 337 401 334 506
33 230 230 220 220 220 220 220 230 240 250 260 260 260 260 260 260 260 260 260 26	15.5 15.1 15.0 15.0
227 209.5 206.5 206.5 148 146 132.5 132.5 125.5 119.5 1115.5 115.5 115.5 1115.5	108 107 105 104.5 104
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## ALIGNMENTS

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SUL JL8		E FROM N.A. BALB/C; S., Liao L S., Liao L Slucosamine cd (NOV-199 F206024; AA	SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64; UBLY MATCh 64.3%; Score 447; DB 11; Length 104; aset Local Similarity 80.8%; Pred, No. 4.3e-38; Atches 84. Conservative	LSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPG	OY 89 GSGSGTDFTLKISTIKPEDLGMYYCLQGTHOPYTFGGGTKLEIK 132 
	•			~ -	J 1

114 AA.

PRT;

PRELIMINARY;

RESULT 2 Q9UL80 ID Q9UL80 AC Q9UL80;

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STRAIN-BALB/C; TISSUB-SPLEEN;
shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
method.";
                                                                                                                                                                                                             01-MAY-2000 (TIEMBLEEL 13, Last sequence update)
01-0CT-2000 (TIEMBLEEL 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.1%; Score 334.5; DB 4; Length 108; 57.1%; Pred. No. 1.1e-26; attive 19; Mismatches 24; Indels 5.
                             57 TGIPDRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
          SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara (N. Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CILL. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; IREI.
INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 1.
                                                                                                                                                         108 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
                                                                                                                                                                               09UL77;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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CN 8.
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NON_TER
SEQUENCE
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090YF0
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Q9UL77
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DVVVTQ PLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).

Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9f 06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                  Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 SGVPDRF3GSGSGTDFTLKISTIKPEDLGMYYCLQGTH-QPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.2%; Score 356; DB 4; Length 109; 58.9%; Pred. No. 7.6e-29; ive 23; Mismatches 19; Indels
                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
WH X., Liu B , Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu E., Van der Merwe P.L., Kalis N.N., Berney S.M. Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA; 11646 MW; SF675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 59.4%; Score 412.5; DB 4; Local Simi.arity 69.9%; Pred. No. 1.5e-34; Les 79; Conservative 15; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immuncl. Immunopathol. 87:184-192(1998).
EMBL. AF035(36; AAD56272.1; -. HSSP, P01785; IMCP.
INTERPRO; IF R003006; -.
                                                                                                                                                                                                                                                                                                        Clin. Immuno... Immunopathol. 87:184-192(1998).
EMBL; AF0350:4; AAD56270.1; -
INTERPRO; IPH003006; -
PFAM; PF0004"; ig; 1.
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MEDLINE=98277139; PubMed=9614934;
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Best Local Sim:larity 58.99
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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NON_TER 109 109
SEQUENCE 109 AA; 116
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Q9UL78 Q9UL78;

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Query Match

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              090L70 PRELIMINARY; PRT; 108 AA.
090L70;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                        Gaps
                                                                                                                                          19 GGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                    226 LADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCOHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                                                       79 RFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                        5,
                                                                                               47.0%; Score 326.5; DB 11; Length 298; 53.5%; Pred. No. 2.5e-25; Indels 5; Mismatches 29; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%; Score 326; DB 4; Length 109;
11arity 54.5%; Pred. No. 8.3e-26;
Conservative 25; Mismatches 22; Indels
      EMBL/GenBank/DDBJ databases.
Bubmitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB036341; BAA88633.1; -.
HSSP; PO1607; 1REI.
INTERPRO; IPR003006; -.
PFAM; PF00047; 1g; 2.
SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035028; AAD56264.1; -.
HSSP; P01789; IMCP.
INTERPRO; IPR003006; -.
NOM-FER. PF00047; 19; 1.
                                                                                                                                                                                                                                                                          109 AA
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                            Query Match
Best Local Similarity 53.5%
Matches 61; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
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Young D.C.;
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NON_TER
SEQUENCE
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09UL86;
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STRAIN-BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmne myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206032; AAF69330.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 LPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFSGS
                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

46.0%; Score 319.5; DB 11; Length
Best Local Similarity 59.8%; Pred. No. 3.4e-25;
Matches 61; Conservative 17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                         108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AA; 10939 MW; 3B25D0E784533324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 323.5; DB 4;
56.2%; Pred. No. 1.5e-25;
tive 17; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
PETRRERO; IPR003006; -.
PETAM; PF00047; ig; 1.
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                                                               SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
  Mammalia;
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Malkiel S., Liao L., Cunningham M.W., Diamond B.,
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF206026; AAF69224.1;
NON_TER
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103 103
SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64:
                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNGELOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQ-GTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                              MEDLINE-98277139; Pubmed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.3%; Score 315; DB 4; Length 109; 53.1%; Pred. No. 1.1e-24; Live 26; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD36029; AAD56265.1; -.
INTERPRO; IREI.
INTERPRO; IPRO03006; -.
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Q9UL85
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Wilde K.G., (u X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., (u X.) Ekramoddoullah A.K.M., Misra S.;
"Cloning of 'DNss encoding for anti-white pine blister rust monoclonal
antibody (Man 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (M1x-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFL52371; AAD40242.1;
FSSP; P01788: IMCP.
                                   01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TERBALCEL. 13, Last sequence update)
01-CCT-2000 (TERBALCEL. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 DVVVTQT1'LSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|:||: | | ||:|:||| || || ||:
| DIVWIOSPSLEASTGDRVIISCRMSQGI-----SSYLAWYQQKPGKAPELLIYAASTLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eu:heria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                     Myosin-reactive autoantibodies in rheumatic carditis and, normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 SGVPDRF: GSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 SGVPSRF:GSGSGTDFTLTISCLQSEDFATYXCQQYXSFPPTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 46.0%; Score 319.5; DB 11; Length Best'Local Similarity 52.7%; Pred. No. 8.6e-25; Matches 59; Jonservative 24; Mismatches 24; Tndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 TrEMBLrel. 13, Created)
01-MAY-2000 TrEMBLrel. 13, Last sequence update)
01-OCT-2000 TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 46.0%; Score 319.5; DB 4; al Similarity 57.1%; Pred. No. 3.8e-25; 64; (Conservative 15; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF0350:5; AAD56271.1; -.
HSSP; P01607; IREI.
INTERPRO; IFF 003006; -.
NON_TER 1 1.
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01-0CT-2000 TrEMBLrel. 15, Last ann
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS03290; IG_MHC; UNKNOWN_1
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
11787 MW;
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                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA;
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Best Local Simi]arity
Matches 64; (Onserv
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                Gaps
                                                                                                            30 SLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFSG 89
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                              1;
                         45.3%; Score 314.5; DB 11; Length 103; 58.3%; Pred. No. 1.1e-24; Live 16; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 44.8%; Score 311.5; DB 4; Length 108; I Similarity 51.8%; Pred. No. 2.4e-24; 58; Conservative 27; Mismatches 22; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGIPARESGSGSGTEFTLTISSLOFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035031; AAD56267.1; -.
INTERPRO; IREI.
INTERPRO; IPR003006;
                                                                                                                                                                                                                                                                                                                                                               108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                           Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
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SEQUENCE
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Matches 5
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Q9UL81;
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                                                                                                                                                                                                                                                                                                               RESULT 13
Q9UL83
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schistosoma japonicum (Blood fluke).
Eukaryota, Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
Strigeidida: Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MONOCLONAL ANTI-IDIDOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Song X.T., Feng 2.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum."
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
HSSP; PO1679; ZFBJ.
INTERPRO; IPR003006; -.
Young D.C.; ^{\prime} Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 VPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.4%; Score 295; DB 5; Length 106; Best Local Similarity 51.8%; Pred. No. 1.1e-22; Matches 57; Conservative 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                              44.6%; Score 310; DB 4; Length 10 llarity 54.5%; Pred. No. 3.4e-24; Conservative 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                        107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AA; 11478 MW; F20F544426BAE63E CRC64;
                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035033; AAD56269.1; -
HSSP: P80362; 1WTL.
PITERREO; IPR003006; -
PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AA.
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                                                                                                                                                                                                                              107
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Best Local Similarity
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us-08-700-737-12.rspt

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us-08-700-737-12.rag

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Murine Act-1 light
Consensus protein
Light chain of a h
3F4 Human 1964 exp
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Monoclonal antibod
MAD 1A7 light chai
Light chain variab
Plasmid pGEM-MIL m
                                                                                                                       April 13, 2001, 15:35:37 ; Search time 57.59 Seconds (without alignments) 131.022 Million cell updates/sec
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Variable kappa cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                  1 MKLPVRLLVLLFWIPVSGG........CLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **Contesteq_401:**

**Contesteq_401:**

**SIDSI/gcgdata/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/AA1985.DAT:**

**SIDSI/gcgdata/geneseqp/AA1985.DAT:**

**SIDSI/gcgdata/geneseqp/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/geneseqp/AA1981.DAT:**

**SIDSI/gcgdata/geneseqp/geneseqp/AA1991.DAT:**

**SIDSI/gcgdata/geneseqp/geneseqp/AA1991.DAT:**
                                                                                                                                                                                                                                                                                                                                                                                                                                       390729
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   390729 seqs, 57163235 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      using sw model
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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W53817
W53812
W14942
W14937
W14937
W21545
Y21545
Y228468
B23812
                                                                                                                                                                                                                US-08-700-737-12
695
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                   OM protein - protein search,
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                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                 Run on:
                                                                                                                                                                                                                       Title:
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No.
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Murine KC-4 immuno Murine KC-4 immuno VL sequence of ant Mouse immunoglobul Chimeric MAD light BRSS-2 light chain	int ant ant egi	Anti-human Fas mon Anti-human Fas ant Plasmid pGEM-M2L Variable 140ht cha R6-5-D6 anti-ICAM- Murine BraficAM- Murine BEE3 immun	light chilight chilight chilight chiligh ICR-8. antibody again antibo ICR-8. ICR-8.	Murine antibody IC Murine antibody IC Humanised murine Mouse Co-1 light c Amino acid sequenc Murine anti-ICAM m Anti-human Fas hum
772 790 157 116 241	227 227 237 237 237 237 237	28887 2888 2888 2088 2088	244844 448144 448144	7443 806 060 219 876
R527 R704 Y174 R322	R322 R528 W608 Y802 W317	W71889 B12909 B23814 W68492 R15199 R11598 R52788	W062 W761 W712 W012 W814	Y8244 Y5075 R5280 W8506 W5021 R1505
15 16 20 14 14	112 113 113 113 113	12 112 113 113 113 113 113	750 750 750 750 750 750 750 750 750 750	221 12 12 13 13
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444444 33000000000000000000000000000000		35. 35. 35. 27. 19.	517.5 517.5 517.5 513 513 513 513	
12 13 14 15 16	18 22 23 23 23 23	3 3 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 4 4 4 4 4 4 4 2 0 0 4 4 4 4 2 4 4 4 4

## ALIGNMENTS

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Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
inflammatory bowel disease.
                                                                             Murine Act-1 light chain variable region.
                                                                                                                                                                                             /note= "signal peptide"
21..132
/note= "mature protein"
                                                                                                                                                                              Location/Qualifiers
                   W53814 standard; Protein; 132 AA.
                                                                                                                                                                                                                                                                             97WO-US13884
                                                                                                                                                                                                                                                                                              96US-0700737
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                 (LEUK-) LEUKOSITE INC
                                                        14-JUL-1998
                                                                                                                                                                                                                                    WO9806248-A2
                                                                                                                                                                                                                                                                            06-AUG-1997;
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                                                                                                                                                                                      Peptide
                                                                                                                                                                                                          Protein
                                       W53814;
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RESULT
W53814
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15-AUG-1996;
                                                          Saldanha J;
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                                                MM,
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                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                 Bendig
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
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                                                                                                                     The present Hequence represents the light chain varaible region of murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Musicosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of th.s particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high andothalial 'emules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                              61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                          Consensus protein sequence of the murine variable light chain region.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       1 MKLPVRLJVLLEWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse, Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised artibody; murine antigen binding region; inhibition; leukocyte irfiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                   Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graff. versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                               Length 132;
                                                                                                                                                                                                                                                                                                     Indels
  Ringler DJ;
                                                                                                                                                                                                                                                                              ; Score 695; DB 19;
; Pred. No. 3e-48;
0; Mismatches 0;
  Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..20
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W53817 standard; Protein; 140 AA.
  Newman W,
                                                                                                        Claim 23; Fig 7; 145pp; English
                                                                                                                                                                                                                                                                                Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 132; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US13884
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                                                                                                                                                                                                                                                                                                                                                                                                          121 YTFGGGTKLEIK 132
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    cones ST,
                                WPI; 1998-15:172/14.
N-PSDB; V200;7.
                                                                                                                                                                                                                                                    1 12 AA;
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    Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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The present sequence represents the consensus amino acid sequence comprising the variable region of murine Act-1 antibody determined from comprising the variable region of murine Act-1 antibody determined from several independent mouse light chain variable region clones. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadcAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to madcAM-1, which is present of high endothelial venules in mucosal lymph nodes. Variable regions were amplified from DNA encoding Act-1 using degenerate PCR primers V20083-84. The degeneracy of the PCR primers V20083-84 is the degeneracy of the PCR primers Consensus sequence, the present sequence was used to construct consensus sequence. The present sequence was used to construct chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit and infaltration of tissues, e.g. for treating inflammatory diseases such as infiltration of islammatory bowel diseases. The immunoglobulin can also be used for an infiltration is a infiltration and islammatory diseases such as infiltration with allowed the immunoglobulin can also be used for an infiltration of the interval of the inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse: Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                          Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain of a humanised murine Act-1 antibody.
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100.0%; Pred. No. 3.2e-48;
tive 0; Mismatches 0;
                                                                                                                                                                          Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection, isolation and diagnosis.
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                                                                                                                                                                               Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
96us-0700737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3; 145pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YTFGGGTKLEIK 132
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                                                                                       (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                                                                                       WPI; 1998-159172/14.
N-PSDB; V20086.
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1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain (W14941) and light chain (W14942) sequences correspond to murine anti-porcine soluble vascular cell adhesion molecule (VCAM) mnoclonal antibody 374 (see also W1493738). They are encoded by a 3F4 human 1gG4 expression plasmid insert (see also T62938). A chimeric antibody specific for porcine VCAM can be produced in transfected host cells. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human
                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                Xenotransplantation; graft rejection; cell interaction; pig vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenotransplantation; graft rejection; cell interaction; plg; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                Rollins S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

80.5%; Score 559.5; DB 18; Length
Best Local Similarity 81.1%; Pred. No. 3e-37;
Matches 107; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine anti-porcine VCAM 3F4 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 65-66; 105pp; English.
                                                                                                                                                                                                                                                                                                              Matis LA, Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W14937 standard; Protein; 238 AA.
                                                                                                                                                                                      96WO-US15575
                                                                                                                                                                                                                       96US-0004489
95US-0004489
                                                                                                                                                                                                                                                                          (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftfgggtkleik 131
                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-212855/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA;
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T62938
                                                                                                                WO9711971-A1
                                                                                                                                                                                     27-SEP-1996;
                                                                                                                                                                                                                   26-SEP-1996;
28-SEP-1995;
                                                                                                                                                    03-APR-1997.
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                                                                                                                                                                                                                                                                                                            Evans MJ,
Rother RP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recipients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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              à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the light chain of humanised murine multbody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadGAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadGAM-1, which is present of high endothelial used to inhibit the interaction of cells bearing alpha4-beta7 with calls bearing alpha4-beta7 with leukcoyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised immunoglobulin reactive with alpha-4-beta-7 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3F4 Human IgG4 expression plasmid insert product (light chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
                                                                                                                                                                                                                                                                                                                                       Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 608; DB 19; )
87.1%; Pred. No. 2.4e-41;
tive 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                    Ponath PD,
                                                                          /note= "signal peptide"
21..138
                                                                                                                       /note- "mature protein"
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Jones ST, Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Fig 12; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W14942 standard; Protein; 238
                                                                                                                                                                                                                            97WO-US13884
                                                                                                                                                                                                                                                               96US-0700737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.1
Matches 115; Conservative
                                                                                                                                                                                                                                                                                               (LEUK-) LEUKOSITE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| |||:|||
|21 ytfgggtkveik 132
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-159172/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V20075
Mus sp.
Homo saplens.
                                                                                                                                                      WO9806248-A2
                                                                                                                                                                                                                         06-AUG-1997;
                                                                                                                                                                                                                                                           15-AUG-1996;
                                                                                                                                                                                                                                                                                                                            Bendig MM,
Saldanha J;
                                                                                                                                                                                        19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                    Peptide
                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W14942;
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(first entry)

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Variable region coding sequence; constant region epitope; hybridoma; antibody detection; antigen/antibody complex; variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                        Use of antibody constant region epitope(s) - as control or calibrator reagents in assays for detecting the presence of
                                                    Variable kappa chain of antibody from hybridoma 1-706-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 62-63; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           antibody in a test sample
                                                                                                                                                                                                                                                                                                                   Golden AM, Hackett JR,
                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-393833/36.
                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T98835.
                                                                                                                                                                                                                             17-JAN-1997;
                                                                                                                                                                                                                                                           23-JAN-1996;
                                                                                                                                                                   W09727486-A1
                            19-MAR-1998
                                                                                                                                        Mus musculus
                                                                                                                                                                                                 31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
W34518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain (W14937) and heavy chain (W14938) sequences are provided for the murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAD) 3F4. Hybridoma 3F4 was produced by standard techniques using recombinant, soluble porcine VCAM as immunogen. Chimeric antibodies can be produced by cloning vCAM as immunogen. Chimeric antibodies can be produced by cloning constant region in place of the human gammal C1 regions into constant region in place of the human gammal C1 region. Sequences can provided for 3F4 (chimeric) human G2/G4 cDNA (W14939), a 3F4 human G2/G4 expression plasmid insert product (W14940), and 3F4 human IGG4 expression plasmid insert products (W14941, 42). The chimeric antibodies are specific for porcine VCAM. They are useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLPVRILVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies binding to porcine but not human cell interaction proteins - seful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 559.5; DB 18; Length 238; pred. No. 3e-37; 9; Mismatches 15; Indels 1;
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                                                                                                                                                                                                                                                                                                                         Rollins
                                                                                                                                                                                                                                                                                                                           Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 52-53; 105pp; English.
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Mitis LA, Mueller EE,
                                                                                 74..80
/label= CDR2
113..121
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.5%;
81.1%;
                                                 43..58
/label= CDR1
                                                                                                                                                                                                                        96WO-US15575
                                                                                                                                                                                                                                                     96US-0004489
95US-0004489
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Best Local Similarity 81.1
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            into human recipients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftfggg:kleik 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YTFGGGTKLEIK 132
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N-PSDB; T62934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AA;
                                                                                                                                                                                                                        27-SEP-1996;
                                                                                                                                                                                                                                                   26-SEP-1996;
28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                              WO9711971-A1
                                                                                                                                                                                           03-APR-1997
                                                                                                                                                                                                                                                                                                                                             Rother RP;
                                                                                                                                                                                                                                                                                                                              Evans MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                    Region
                                                                                                                   Region
                                                         Region
            Mus sp
                                           Key
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an

Ostrow DH;

Hoff JA,

97WO-US01074. 96US-0589939.

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This sequence represents the variable kappa chain of the antibody of produced by hybridoma 1-706-139, and can be detected using the method of produced by hybridoma 1-706-139, and can be detected using the method of the invention. The method is for detecting the presence of antibody which can be present in a test sample. It comprises contacting a test sample can suspected of containing the antibody with an antigen specific for the can produce of the antibody which may be present in the test sample and the presence of the antibody which may be present in the test sample and can the presence of the antibody which may be present that the can control or calibrator, a reagent which binds to the antibody constant region epitopes, where the reagent binds to the antigen antibody constant region epitopes, where the reagent binds to the antigen can be also be used for detecting the presence of antibodies developed can be also be used for detecting the presence of antibodies developed against more than one antigen. The method is used particularly for the epaticular of the problems associated with using an immune sera in the manufacture of the problems associated with using an immune sera in the manufacture of calibrators and positive controls. The present reagents can be readily and reproducibly generated in virtually unlimited quantities and are also useful for quantitating, and monitoring the integrity of, the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.4%; Score 558.5; DB 18; Length 131; 81.1%; Pred. No. 1.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.4
Best Local Similarity 81.1
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YTFGGGTKLEIK 132
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W34518 TD W34518 standard; Protein; 131 AA.

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The present sequence is that of the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the anti-gangiloside 2 (GD2) MAb 1GC2a, which binds an unique eptope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroectodermal tumours, e.g. malignant melanoma, neuroblastroma, glotoma, soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its CDNA can be used in a vaccine to treat or palliate such diseases. They can also be used to reduce the risk of recurrence of a clinically detectable tumour, and detect an anti-GD2 Ab bound to a tumour cell.

MAb 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoral response) and
                                                                                                                                                                                                                                                         Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7; variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma; glycosphingollpid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.58
/note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region 3"
                                                                                                                                                                                                          Anti-idiotype monoclonal antibody 1A7 variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122..131
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59..73
/note= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..112
ote= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
                                              W03199 standard; Protein; 149 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                     amplification; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US00882
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                                                                                                                                                   26-FEB-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T31332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9622373-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-1996;
17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                     W03199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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RESULT
                        W03199
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                                                                                                                                                                                                                                                                                                                                                   61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Psoriasis; immunological response; anti-idiotype antibody; gluttate; chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis; monoclonal antibody; 1A7.
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                           1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                               The CDNA can be used in expression systems for IA7 prodn., and in the prepn. of probes and primers to respectively assay for IA7
                                                                                     the prepn. of probes and primers to respectively assay for IA7 CDNA, and amplify desired polynucleotides for use in gene therapy
GD2-specific cells (cellular response). It can be used to purify anti-1A7 (Ab3), anti-6D2 (Ab1') or 14G2a (Ab1), detect anti-1A7 or anti-6D2 in a sample or measure the level of cellular anti-1A7 or anti-GD2 activity.
                                                                                                                                                                                                                                ä
                                                                                                                                                                                           DB 17; Length 149;
                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody 1A7 light chain variable region.
                                                                                                                                                                                          79.8%; Score 554.5; DB 1
79.5%; Pred. No. 4.6e-37;
.ive 10; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y21545 standard; Protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KENT ) UNIV KENTUCKY RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                        Best Local Similarity 79.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chatterjee M, Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treatment of psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                  121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-347407/29
                                                                                                                                        149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; X60629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                          Sequence
                                                                                                                                                                                          Query Match
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Gaps

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Indels

Length 149;

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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                           Light chain variable region; antibody 147; T cell response; melanoma; ganglioside GD2; CDR; complementarity determining region; carcinoma.
                                                1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                              20. 149
/label= "mature peptide"
/note= "light chain variable region of Ab 1A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining Region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity Determining Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complementarity Determining
    Score 552.5; DB 20;
Pred. No. 6.6e-37;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132.149
/label= "Constant region"
                                                                                                                                                                                                                                                                                                                                                                                                   1..19
/label= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122..131
/label= "Framework 4"
132..149
                                                                                                                                                                                                                                                                                                      Light chain variable region of MAb 1A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..42
/label= "Framework 1"
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                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59..73
/label= "Framework
                                                                                                                                                                                                                                  Y28468 standard; Protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43..58
/label= "CDR 1"
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/label= "CDR 2"
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/label= "CDR 3"
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95US-0372676.
96US-0591196.
    79.5%;
ilarity 79.5%;
Conservative
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                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                              121 YTFGGGTKLEIK 132
                 Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1995;
16-JAN-1996;
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        Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                          Y28468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a monoclonal antibody (MAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 - associated liseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the light chain variable region of MAb 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody lA7 which elicits an anti-GD2 immunological response, us=ful for the development of products for the detection and treatment of cancers -
                                                                                                                                                   61 YLHKPGQ(:PQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                               Gaps
                                                                                                   1 MKLPVRLIVLLEWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                   Monoclonal autibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastomu; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen.
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                                                        Length 149;
                                                                               Indels
                                                                               16;
                                                         DB 20;
chain variable region of monoclonal antibody 1A7
                                                        Score 554.5; DB 2 Pred. No. 4.6e-37;
                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chatterjee M;
                                                                                                                                                                                                                                                                                                                                                           MAb 1A7 ligh: chain variable region
                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                     Y49209 standard; Protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 74pp; English.
                                                        Query Match 79.8%;
Best Local Similarity 79.5%;
Matches 105; Conservative 1
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                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chitterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KENT ) UNIV KENTUCKY
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120 wtfgggtl:leik 131
                                                                                                                                                                                                   121 YTFGGGTHLEIK 132
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N-PSDB; Z31355.
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                       149 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                             X49209;
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cells having integrin associated protein for treatment of
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                   present invention.
                                                                                                                                                                       131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1995
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                                                                                                                                                                       Sequence .
               leukemia
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                                                                              This polypeptide is the variable light chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide has three CDRs (complementarity determining regions) and four frame work regions. When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The heavy chain variable region of the 1A7 mantibody (Y28469) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T call and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and neuroblastoma, glioma, soft tissue sarcoma, and small cell lung cancer).
                                                                                                                                                                                                                                                                                                                                   61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                               1 MKLPVRLLVLLEWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                       Single stranded Fv antibody fragment inducing apoptosis in nucleated
                             Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pGEM-M1L mouse MABL-1 L chain V region protein SEQ ID NO:5.
                                                                                                                                                                                                                                                   Score 552.5; DB 20; Length 149;
Pred. No. 6.6e-37;
9; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; MABL; IAP; integrin associated protein; single stranded Fv; apoptosis; blood disease; leukaemia; cytostatic.
                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   B23812 standard; Protein; 131 AA.
                                                            Claim 1; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                   79.58;
79.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2001 (first entry)
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                                                                                                                                                                                                                                                                       Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        121 YTFGGGTKLEIK 132
WPI; 1999-457600/38.
N-PSDB; X89552.
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                     Sequence 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200053634-A1.
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The present invention describes a polypeptide containing the variable region of the light chain of a monoclonal antibody, which induces apoptosis, in nucleated blood cells having integrin associate protein (IAP). Also described are: (1) DNA encoding the novel polypeptide; (2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the polypeptide. The polypeptide can be used in the treatment of blood disorders such as leukaemia. The present sequence represents the plasmid pGRM-NIL mouse MABE-11, chain V region which is given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine KC-4 immunoglobulin light chain variable region (deduced).
                                                                                                                                                                                                                                                                                                                                                                                      Length 131;
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/note= "putative glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                   Score 550.5; DB :
Pred. No. 8.3e-37.8; Mismatches 1
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/label= KC-4_mature_VL-chain
Claim 4; Page 50-51; 73pp; Japanese.
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/label= CDR3
122..131
/label= FR4
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/label- FR2
74..80
/label- CDR2
81..112
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/label= CDR1
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/label= CDR1

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(CANC-) CANCER
                                                                    Modified-site
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30-SEP-1993;
08-OCT-1993;
                                                                                                                                                                                      16-NOV-1993;
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                                                                                                                                                                  26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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        Region
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R70457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLHKPGQ SPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLPVRL:VLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4.
                                                                                                                                                                                                          An initial isolation of cDNAs coding for murine anti-human breast carcinoma MAD KC-4 was performed using PCR with commercially swallable pr.mers (see Q62751-062758, wasilable from NOVAGEN). Subsequent c.oning using PCR primers JO20, JO21, JO22 and JO24 (see Q62759-062762) resulted in the isolation of the mouse Ig variable downins. The amplified cDNAs were sequenced (Q62763 and Q62764) and imino acid sequences were deduced from them. Chimeric mouse-human intibodies were constructed using human constant regions so as to produce less immunogenic polypeptides which retained the anti-human carcinoma binding specificity of KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine KC-4 immunoglobulin light chain variable region (deduced).
                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                             Chimeric human-murine polypeptide(s) specific for human mammary fat globule antigen - for imaging, diagnosing and treating neoplasia, with less undesirable immunogenic response
                                                                                                                                                                                                                                                                                                                                                         DB 15; Length 131;
                                                                                                                                                                                                                                                                                                                                                         78.9%; Score 548.5; DB 15; Length 78.8%; Pred. No. 1.2e-36; ive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20..131
/label= KC-4_mature_VL-chain
                                                                                              (CANC-) CANCHR RES FUND CONTRA COSTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                          Example 27; Page 41; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R52790 standard; Protein; 131 AA.
                                                   92US-0977706.
92US-0977707.
93US-0128015.
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                               93WO-US11316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                           Query Match 78.9%
Best Local Simi.arity 78.8%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20..42
/label= I
43..58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGT (LEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-18::509/22.
                                                                                                                                                                                                                                                                                                                             1 11 AA;
                                                                                                                             N-PSDB; Q62763.
                                                   13-NOV-1992;
13-NOV-1992;
28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1995
                                 15-NOV-1993;
           26-MAY-1994
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R52790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An initial isolation of cDNAs coding for murine anti-human breast carcinoma MAb KC-4 was performed using PCR with commercially available primers (see 662776-662783, available from NOVAGEN). Subsequent cloning using PCR primers 7020, J021, J022 and J024 (see 662784-062787) resulted in the isolation of the mouse Ig variable domains. The amplified cDNAs were sequenced (062788 and 062789) and amino acid sequences were deduced from them. Chimmerc mouse-human antibodies were constructed using human constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions so as to produce less immunogenic polypeptides which retained the anti-human carcinoma binding specificity of KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New analogue peptide(s) comprising antibody variable regions used to develop prods. for use in the detection, diagnosis, therapy and prevention of neoplasms
                                                                                                                                                                   "putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ceriani RL, Do Couto FJR, Padlan EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RES FUND CONTRA COSTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 26; Page 61; 109pp; English.
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                                                                                                                                                                   putat
113..121
/label= CDR3
122..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0977696.
93US-0129930.
93US-0134346.
59..73
/label= FR2
74..80
                                                74..80
/label= CDR2
                                                                                            81..112
/label- FR3
98..100
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/label= FR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-183510/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                           were prepared by PCR from Dolyadenylated RNA isolated from 100 million KC-4 hybridoma cells. All clones were obtd. from independent PCRs. The sequences of the primers are given in Q87519-Q8756. The sequences of the primers are given in Q87519-Q8756. Independent its derived protein sequenced, without prior purificn., into pCR1000 its derived protein sequenced in both directions. The VL DNA sequence and its derived protein sequences are shown in Q87531 and R70449-R70457. The mature VL chain begins at AA D of framework i (FRI). VL is a group II kappa chain. Part of the CDR3 and all of the FR4 are encoded by JK2. There is a an asparagine glycosylation site in the sequence of R70449-R70456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                    cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
                                                                                                                                                                                                                                      New humanised anti-KC-4 monoclonal antibody - used for detection cancer cells, in vivo imaging, ex-vivo purging and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ı;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 548.5; DB 16; Length 131; Pred. No. 1.2e-36;
                                       Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
                   VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                               (CANC-) CANCER RESEARCH FUND CONTRA COSTA,
                                                                                                                                                                                                                                                                             Example; Table 14, Page 31; 61pp; English.
                                                                                                                                                                                      Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse immunoglobulin E light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y17416 standard; Protein; 238 AA.
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                                                                                                                                             93US-0134346
                                                                                                                         93WO-US11444
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1999 (first entry)
                                                                                                                                                                                    Ceriani RL, Docouto JJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.89
Matches 104; Conservative
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                                                                                                                                                                                                        WPI; 1995-161912/21
                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA;
                                                                                                                                                                                                                   N-PSDB; Q87531
                                                                                                                        16-NOV-1993;
                                                                                                                                          08-OCT-1993;
27-0CT-1995
                                                                               W09510776-A.
                                                                                                   20-APR-1995
                                                            Synthetic.
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The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is substances i.e. with antiallergic activity and the ability of substances i.e. with antiallergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IgE) light chain, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.6%; Score 546.5; DB 20; Length 78.0%; Pred. No. 3.2e-36; Live 11; Mismatches 17; Indels
                                                                                          /label- signal
20..238
/label- immunoglobulin_E_light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taya C, Yonemawa
                                                                                                                                                                                                                                                                                                                                                                                       (SANY ) SANKYO CO LTD.
(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic non-human animal allergy models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 13, 2001, 15:35:39
Job time: 118 sec
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 30-32; 42pp; English
                                                                                                                                                                                                                                                                                                                                           97JP-0313989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuoka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karasuyama H,
                                                                                                                                                                                                                                                                                          13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                           14-NOV-1997;
                                                                                                                                                                                           EP921189-A1
                                                                                                                                                                                                                                          09-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 28;
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                                                Key
Peptide
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April 13, 2001, 17:37:55 ; Search time 4.45 Seconds (without alignments) 51.491 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                    7695 segs, 1735856 residues

    protein search, using sw model

                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   US-08-700-737-12
                                                                                                                                                                                 Title:
Perfect score:
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                                                                      OM protein
                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                         Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Match Length DB Score Result Š.

Appl Appl Appl Appli Appli Appl Appli App11 App11 Appl Appl Sequence 62, Appl Sequence 2, Appli Sequence 11472, A Sequence 4, Appli Appl Sequence 11, 1 Sequence 2, Ap Sequence 334, Sequence 12, 1 Sequence 16, Sequence 11, Sequence 20, Sequence 3, A Sequence 2, A Sequence 22, Sequence 6, A Sequence 15, Sequence 17, Sequence 19, Sequence 6, Sequence 7, Sequence 4, Description Sequence 2 Sequence 6 Seguence Sequence Sequence US-09-808-689-2 US-09-739-449-11472 US-09-509-031-16
US-09-509-031-16
US-09-509-031-6
US-08-475-815A-11
US-09-386-658-4
US-09-386-658-2
US-09-815-108-20
US-09-815-108-2
US-09-815-108-2
US-09-815-108-2
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US-09-815-108-6
US-09-815-108-6
US-09-815-108-6
US-09-815-108-6
US-09-815-108-6 PCT-US01-09226-61 PCT-US01-09226-62 US-09-815-108-17 US-09-815-108-19 US-09-808-689-6 391.5 366.5 357.5 354.5 354.5 304 101 90.5 74 

Sequence 11753 A	Section of the Sectio		Sequence 11033, A		Section 19606				du (or (c ocuentos	Section 6734 Pr	de 'solononono	Sequence 330, App	Sequence 101/0, h		Sequence 9552 An	• •	Sequence 14, Appl
US-09-739-449-11753	US-09-739-449-9355	US-09-739-449-11033	US-09-739-449-8751	US-09-815-108-7	US-09-739-449-12606	US-09-739-449-10896	US-09-739-449-12091	US-09-739-449-9798	US-60-278-037-7	US-09-739-449-9734	115-09-809-391-396	US-09-739-449-13176	US-09-739-449-10487	US-09-739-449-11965	US-09-739-449-9552	US-09-808-689-10	US-09-808-689-14
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. 60	28	57.5	57.5	57.5	57	56.5	56.5	26	26	55.5	55	55	54.5	54	24	24	54
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington SOFTWARE: PatentIn Release #1.0, Version #1.25 Bruce, Kim Folger
Schreiber, George J.
Siegall, Clay
McAndrew, Stephen
TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN NAME: ROSenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 840065.405D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-691
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,504
FILING DATE: 12-Feb-2001
CLASSIFICATION: CURNOWN>
ATTORNEY/AGENT INFORMATION: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-782-504-4 APPLICANT: Hellstrom, Ingegerd Hellstrom, Karl Erlk Sequence 4, Application US/09782504 GENERAL INFORMATION: LENGTH: 240 amino acids TYPE: amino acid ZIP: 98104 COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 4 COUNTRY: USA RESULT 1 US-09-782-504-4

Gaps 6 Length 240; Indels Ouery Match 56.3%; Score 391.5; DB 5; Best Local Similarity 70.6%; Pred. No. 9.1e-34; Matches 84; Conservative 10; Mismatches 16;

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APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabrielt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 70; Conserv
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US-09-509-031-6
                                                                                                                                                                                              US-09-509-031-11
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US-09-509-031-6
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REPERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT APPLICATION NUMBER: US/09/509,031
SUFFERENCE FILING DATE: 2000-06-09
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                             APPLICANT: Sucss, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATCHILIN Ver. 2.1
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORM/TION: Description of Artificial Sequence:ccMTLgL protein; OTHER INFORM/TION: sequence
US-09-509-031-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GGDVVVT )TPLSLPVSFGDQVSISCRSSQS-LAKSYGNTYLSWYLHKPGQSPQLLIYGIS 77
SGG----IVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLI 73
                                                                     74 YGISNRF&GVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence: CATAB-TEV CTHER INFORMATION: protein sequence US-09-509-031-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%; Score 366.5; DB 5;
Larity 62.6%; Pred. No. 7.4e-31;
Conservative 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.4%; Score 357.5; DB 5; Best Local Similarity 61.2%; Pred. No. 5.8e-30; Matches 71; Conservative 17; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09509031 GENERAL INFORMATION:
                                                                                                                                                                                                 Sequence 4, App.ication US/09509031
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
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Best Local Similarity (
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                                                                                                                                                                     RESULT 2
US-09-509-031-4
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GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tariliton, David M.
APPLICANT: Tariliton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
                      A METHOD OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DVVVTQTPLSLPVSFGDQVSISCRSSQS-LAKSYGNTYLSWYLHKPGQSPQLLIYGISNR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 GGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGN--TYLSWYLHKPGQSPQLLIYGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
                                                                                   SNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 FSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Kappa
; OTHER INFORMATION: protein sequence
US-09-509-031-11
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Pred. No. 3.1e-30;
Mismatches 26;
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Pred. No. 7.8e-30;
                                                                                                                                                                                                                                                                                                APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A M.
FILE REPRENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFWMARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
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CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                       ; Sequence 11, Application US/09509031; GENERAL INFORMATION:
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61.9%;
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ilarity 61.9%;
Conservative 10
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APPLICANT: Hanna, Nabli A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reft Mitchell E.
APPLICANT: Reft Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: THERAPBUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: LYMPHONA
TITLE OF INVENTION: LYMPHONA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
          55 HWFQQKPGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 109;
                                                                                                                                                                                    Sequence 4, Application US/09386658
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JPW/SHS/MYM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.7%; Score 303.5; DB 5;
52.7%; Pred. No. 3e-25;
Live 19; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PILLSBURY WINTHROW STREET: 1100 New York Avenue, N.W., Ninth FL. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PULCA APPLICATION DATA:
PAPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08475815A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Anderson, Darrell R.
: Hanna, Nabil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995
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APPLICATION NUMBER: US
                                                  119 OPYTFGGGTKLEIK 132
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
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Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: mouse
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US-08-475-815A-11
                                                                                                                                                RESULT 7
US-09-386-658-4
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APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: THERAPUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
MITTLE OF INVENTION: LYMPHOMA
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      Gaps
                                 21 DVVVTQTPLSLPVSFGDQVSISCRSSQS-LAKSYGNTYLSWYLHKPGQSPQLLIYGISNR 79
                                                            59 SWYLHKPGOSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTH 118
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                                                                                                                                        Length 128;
    26; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: PILLSBURY WINTHROP
1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 304; DB 4;
Pred. No. 3.3e-25;
2; Mismatches 40
  16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FLIJNG DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                         Sequence 7, Application US/08475815A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.8%; Promatches 64; Conservative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7:
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amino acid
Conservative
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                                                                                                                                                                                                                                                                                                                        Hanna, Nabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202-822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
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  70;
                                                                                                                                                                                                                                  US-08-475-815A-7
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APPLICANT:
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US-08-475-815A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGQSPQIL--IY-----GISNRFSGVPDRFSGSGGGTDFTLKISTIKPEDLGMYYCLQG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PGRGLEV IGAIYPCNGDTSYNQKFKGKATLTADKSSSTAY-MQLSSLTSEDSAVYYCARS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLFWIP/SGG---DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 VLLLFW1PVSGGDVVVTQTPLSLP----VSFGDQVSISCRSSQSLAKSYGNTYLSWYLHK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 90.5; DB 5; Length 132;
; Pred. No. 0.0015;
31; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.4%; Pred. No. 0.00014;
Matches 34; Conservative 26; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Erianger, Bernard
APPLICANT: Clen, Bi-Xing
TITLE OF INVENTION: ANTHBODIES SPECIFIC FOR FULLERENES
FILE REFERENCH:: 05/5-54182/JPW/SHS/AVM
CURRENT FILIN: DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
                                                                                 23522-0157
US 07/978,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
18.-09.386-568-2
Sequence 2, Application US/09386658
GENERAL INFORM.TION:
                                             NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFRENCE/POCKET NUMBER: 2352
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
25.0%;
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
               FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
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Best Local Sim.larity 25.0%
Matches 33; Conservative
                                                                                                                                                                                   : 140 amino acids
amino acid
                                                                                                                                                                                                                                 MOLECULE TYFE: protein US-08-475-815A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ); ORGANISM: mouse [murine]
US-09-386-658-2
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 APPLICATION NUMBER:
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                                                                                                                                                                                                                     TOPOLOGY:
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RESULT 10r US-09-533-077-331

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APPLICANT: POOG, Sherman
APPLICANT: POOG, Sherman
APPLICANT: Audrey Goddard
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: RELATED DISEASES
TITLE OF INVENTION: RELATED DISEASES
CURRENT APPLICATION NUMBER: US/09/808,689
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 TYLSWYLHKPGQSPQLLIYGISNR----FSGVPDRFSGSGSGTDFTLKISTIKPEDLGMY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ---KWKYEKPDGSPVFIAFRSSTKKSVQYDDVPEYKDRLNLSENYTLSISNARISDEKRF 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 RLLVLLLF------WIPVSGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 39
                                                     APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.47865
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 2000-03-22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 70.5; DB 5; 25.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 74; DB 5 22.0%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
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Sequence 334, Application US/09533077
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.6%
Best Local Similarity 22.0%
Matches 27; Conservative
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; ORGANISM: Homo sapiens
US-09-808-689-12
                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens US-09-533-077-334
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Best Local Similarity
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LENGTH: 582
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10.0%;
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US-09-815-108-22
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LENGTH: 529
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GENERAL INFORMATION:
APPLICANT: Sharis, Christiaan M.
APPLICANT: Sharon, Mu X.
APPLICANT: Sharon, Mu X.
APPLICANT: Bone, Thomas Charles
APPLICANT: Covey, Todd
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 99-513-A
CURRENT APPLICATION NUMBER: US/09/815,108
CURRENT FILING DATE: 2001-03-22
FRIOR PPLICATION NUMBER: 60/191,379
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID MOS: 22
NUMBER OF SEQ ID MOS: 22
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                        APPLICANT: SHAW MIN APPLICANT: STATE MIN MIN APPLICANT: APPLICANT: APPLICANT: APPLICANT: Boone, Thomas Charles
APPLICANT: Covey, Todd
TITLE OF INVENTION: Uses Thereof
CURRENT APPLICATION NUMBER: 2001-03-22
PRIOR APPLICATION NUMBER: 60,191,379
PRIOR PLILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 VLTGTHPVNTTVDFGGTTSFQCK----VRSDVKPVIQWL-----KRVEYGSEGRHN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 STIDVGGQKEVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSF 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69.5; DB 5;
Pred. No. 0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
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Pred. No. 1;
               Sequence 20, Application US/09815108
GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
APPLICANT: Sharon, Mu X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%;
24.3%;
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Best Local Similarity 24.3%;
Matches 28; Conservative 1
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Best Local Similarity 24.3%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-09-815-108-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: TRANSMEM
; LOCATION: (355)..(375)
US-09-815-108-3
US-09-815-108-20
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APPLICANT: Sharon, Mu X.
APPLICANT: Ala, Min
APPLICANT: Ala, Min
APPLICANT: Ala, Min
APPLICANT: Booker, Thomas Charles
APPLICANT: Covey, Thomas Charles
APPLICANT: Covey, Thomas Charles
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 99-513-A
CURRENT APPLICATION NUMBER: US/09/815,108
PRIOR APPLICATION NUMBER: 60/191,379
PRIOR FILING DATE: 2000-03-22
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
APPLICANT: Saris, Christiaan M.
APPLICANT: Staron, Mu
APPLICANT: Ata, Min
APPLICANT: Boone, Thomas Charles
APPLICANT: Covey, Todd
TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFRENCE: 99-513-8
CURRENT APPLICATION NUMBER: US/09/815,108
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/11,379
PRIOR FILING DATE: 2000-03-22
PRIOR SPECIAL OF THE SARIA SA
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                                                            270 STIDVGGQKEVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSF 324
82 GVPD----RFSGSGSGTDFT-----LKISTIKPEDLGMYYCLQGTHQPYTF 123
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09815108
GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
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SOFWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENCTH: 594
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CORGANISM: Mus musculus
US-09-815-108-2
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Length 594;

DB 5;

Score 69.5;

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5,
                   Best Local Simi.arity 24.3%; Pred. No. 1.2;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps
                                                οy
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Search completed: April 13, 2001, 17:37:56 Job time: 172 sec

Sequence 10, Applisequence 3, Applisequence 3, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 12, Applisequence 45, Applisequence 66, A

Sequence:

Run on:

Searched:

Database

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APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Singler, Douglas J.
APPLICANT: Saldanha, Jos
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TILLE OF INVENTION: HUMBNIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HUMBNIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP Compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AGG-1996
                                                                                                                                                                                 US-08-20-20-20-08-11
US-08-700-737-52
US-08-286-754-45
US-08-408-724-45
US-08-472-819-45
US-08-487-113C-45
                                                                                                                                                                                                                                                                                 US-09-382-289-45
US-09-046-351-18
US-09-046-351-82
US-08-827-23-82
US-08-827-23-82
US-09-046-351-80
US-08-700-737-50
US-08-700-737-50
US-09-318-661-4
US-08-155-874A-60
                                          US-09-046-351-10
US-09-523-095A-10
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US-08-665-839B-60
US-09-454-925A-10
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US-07-977-707B-11
US-08-128-015-11
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                                                                                                                               US-07-977-706A-11
                                                                                                 US-08-650-108-3
US-09-059-063-9
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US-07-946-314-3
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NAME: BROOK, DBV1d E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-700-737-12
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695
1 MKLPVRLLVLLFWIPVSGG........CLQGTHQPYTFGGGTKLEIK 132
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Sequence 6, 1
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                                                                                          April 13, 2001, 17:37:47 ; Search time 117.03 Seconds
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ptodata/2/paa/US092_COMB.pep:*
ptodata/2/paa/US093_COMB.pep:*
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/cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO7_COMB.pep:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-700-737-6
US-08-700-737-21
US-08-700-737-7
US-09-324-191-2
US-09-293-533-2
US-09-293-533-2
US-08-134-346A-50
US-08-134-346A-50
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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695
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COUNTRY:
                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fingler, Douglas J.
APPLICANT: Fingler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Eendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SECUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                      Length 132;
                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                    100.0%; Score 695; DB 11;
100.0%; Pred. No. 3.3e-61;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: APLICATION DATA:

APPLICATION NUMBER: US/08/700,737
FILING DAT!: 15-AGG-1996
CLASSIFICATION: 435
ATTORNEY/AGET INFORMATION:
NAME: Brock, David E.
REGISTRATICN NUMBER: 22,592
REFERENCE/COCKET NUMBER: LKS95-10
FELECOMMUNIC/IION INFORMATION:
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-9540
SEQUENCE CHAIACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING (YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08700737 GENERAL INFORMFIION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (517) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUIENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type: amiro acids
Type: amiro acids
TOPOLOGY: 1:--
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                                                                                                                               MOLECULE TYPE: protein US-08-700-737-12
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                                                                                                                     TOPOLOGY:
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                                                                                                                                                        61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                              1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ponath, Paul D.
APPLICANT: Bingler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Weaman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                       ;
    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
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                                       Indels
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STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737 FILING DATE: 15-AUG-1996
Score 695; DB 11;
Pred. No. 3.6e-61;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 616; DB 11;
Pred. No. 2.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/CDOCKET NUMBER: LKSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                       0;
  100.0%;
ilarity 100.0%;
Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.6%;
87.9%;
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Best Local Similarity 87.9
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                             121 YTFGGGTKLEIK 132
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                    Best Local Similarity
Matches 132; Conserv
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; Sequence 2, Application US/09293533 ; GENERAL INFORMATION:
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ORGANISM: Mus Musculus
US-09-324-191-2
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US-09-293-533-2
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| Sequence 2, Application US/09192838
| Sequence 2, Application US/09192838
| GENERAL INPORMATION:
| APPLICANT: FOON, Kenneth A.
| APPLICANT: CHATTERJEE, Malaya
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
| FILE REFERENCE: 304142000500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
61 YLOKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQP 120
                                                                                                                            APPLICANT: Ringler, Douglas J.
APPLICANT: Sander, S. Tarran
APPLICANT: Newmen, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Broat
STREET: TWO MINIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 112;
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100.0%; Pred. No. 3.6e-51;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
REGISTATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTATION NUMBER: LESCOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SED ID NO: 7:
CEDITION FOR SED ID NO: 7:
CEDITION FOR SED ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                    121 YTFGQGTKVEIK 132
                                 121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-700-737-7
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GENERAL INFORMATION:
APPLICANT: THE APPLICANT: OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: CHATTERIEE, Malaya
APPLICANT: CHATTERIEE, Nalaya
APPLICANT: CHATTERIEE, Nalaya
APPLICANT: Malaya
APPLICANT: Wenneth A.
FILE REPERENCE: 304142000540
CURRENT APPLICATION NUMBER: US/09/324,191
CURRENT FILING DATE: 1999-06-02
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
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                                                                                                                                                                                                                                                                                                                                              79.8%; Score 554.5; DB 379.5%; Pred. No. 3.2e-47; Live 10; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2e-47
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Best Local Similarity 79.5%; Pred. No. 3.2e
Matches 105; Conservative 10; Mismatches
CURRENT APPLICATION NUMBER: US/09/192,838
CURRENT FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 60/065,774
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SSCTWARE: PatentIn Ver: 2.0
LENGTH: 149
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Best Local Similarity 79.53
Matches 105; Conservative
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ENCODING IT, KIT AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                60 YLQKPGQSPKLLIXKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVP 119
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                      1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
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                                                                                                                                                                                                                                      Score 550.5; DB 19; Length 131;
Pred. No. 7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Diskette-3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,346A FILNO DATE: 08-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/08134346A

SERRRAL INFORMATION:
APPLICANT: do COUTC, F.J.R.
APPLICANT: Ceriani, R.L.C.
TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND FITLE OF INVENTION: DAGNOCLONAL ANTIBODY AND DNA AND NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                              17; Indels
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                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Ostrager, Chong & Flaherty
STREET: 300 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara L.
REGISTRATION NUMBER: 34,889
REFERENCE/DOCKET NUMBER: CLT I
TELECOMMUNICATION INFORMATION:
TELEFONE: 212-826-655
TELEFAX: 212-826-5999
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                        79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 131 amino acids
amino acid
                                                                PatentIn Ver. 2.1
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Best Local Similarity 77.3
Matches 102; Conservative
                                                                                                                                                                                                                                                                                   Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 YTSGGGTKLEIK 131
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                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                        ; ORGANISM: Mus sp. US-09-523-095A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-134-346A-50
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US-08-134-346A-50
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                                                                                                               131
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                                                                                           SEQ ID NO 6
LENGTH: 13
                                                                                                                                      TYPE: PRT
                                                                         SOFTWARE:
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APPLICANT: 'hatterjee, Malaya
APPLICANT: 'hatterjee, Malaya
APPLICANT: 'hatterjee, Sunil K.
APPLICANT: 'hatterjee, Sunil K.
TITLE OF INV.NTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INV.NTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
TITLE OF INV.NTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
TURBER OF SEDJENCES: 66
CORRESPONDEN'E ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 735 PAGE MILL ROAD
CITY: PAL) ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YLHKPG(SPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YLQKPG(SPULLIYFVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVXYCFGGSHVP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLPVRILVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: 010-EDA, MASAYOSHİ
APPLICANT: KIKUCHI, YASUĞUMİ
TİTLE ÖP İNVEHTILINI APOPTOSIS-INDUCING SINGLE-CHAIN FV
FILE REFERRACI: 065678/0102
CURRENT APPLICATION NUMBER: US/09/523,095A
CURRENT FILLIN: DATE: 2000-03-10
PRIOR APPLICANION NUMBER: JP 11-63557
PRIOR FILLIN: DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                                    COMPOUER REAJABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PROG APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NESCUS 50.095A-6
Sequence 6, Aprilication US/09523095A
GENERAL INFORM.TION:
APPLICANT: FUKUSHIMA, Nacshi
APPLICANT: UNIO, Shinsuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 149 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FCR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYFE: protein US-09-293-533-2
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                            COUNTRY: JSA
ZIP: 94301-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: ami
TOPOLOGY:
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US-08-485-044-4
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                                                                                               1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
                                                                         61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP
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thes 17; Indels
                                                                                                                                                                                                                                                                                                                  APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Cerlani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Pedian Dr., Jerry A.
APPLICANT: Pedian Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
GORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: November 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Pretty, Schroeder & Poplawski 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.3%; Score 537.5; Pest Local Similarity 77.3%; Pred. No. 1.4e Matches 102; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P6639938
                                                                                                                                                                                                                                             RESULT 10
US-08-976-288A-95
; Sequence 95, Application US/08976288A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/977,696
FILING DATE: November 16, 1992
ATTORNEY,AGENT INFORMATION:
NAME: VIviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: n.a. INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 131 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-976-288A-95
                                                                                                                                                     121 YTFGGGTKLEIK 132
                                                                                                                                                                       120 YTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Los Angeles
California
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STREET: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                           1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08485044
GENERAL INFORMATION:
APPLICANT: Tsuruo, Takashi
APPLICANT: Hamada, Hirofumi
APPLICANT: Hamada, Hirofumi
APPLICANT: Kurosawa, Yoshikazu
TITLE OF INVENTION: Chimeric Antibody Against Drug-Resistant
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACDESSE:
Campuell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
CAMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: DAM PC COMPATIBLE
OMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/485,044
FLING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
RECHERNCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REPRENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.2%; Score 536.5; DB 8; 78.0%; Pred. No. 1.7e-45; ive 10; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-827-223-10
'Sequence 10, Application US/08827223
'SERERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 amino acids
amino acid
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Best Local Similarity 78.0
Matches 103; Conservative
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                                                                                                                                                                  121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                   120 YTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 RTFGGGTKLEIK 131
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1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60 

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Sequence 10, Application US/09523095A; GENERAL INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
                                                                                                                                                                        77.18;
78.08;
                                                                                                                                                                                                            Conservative
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CRGANISM: Mus musculus
US-09-046-351-10
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SOFTWARE: Patentin Ver.
SEQ ID NO 10
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                         121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                               120 PAFGGGTKLEIK 131
                                                                                             ; ORGANISM: Mus musculus US-08-827-223-10
                                                                                                                                                                                          Best Local Similarity
Matches 103; Conserv
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US-09-523-095A-10
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US-09-046-351-10
                                                                             TYPE: PRT
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                        APPLICANT: ::chikawa, Kimihisa
APPLICANT: :chikawa, Kimihisa
NUMBER OF SENUENCES: 80
CORRESPEDINEN: ADDRESS:
ADDRESSE: Frishauf, Holtz, Goodman, Langer & Chick,
ADDRESSE: P.C.
STREET: 7:7 Third Avenue
CITY: New York
STATE: Nev York
COUNTRY: Jnited States
ZIP: 1001-2023
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Sequence 10, Application US/08827223A

Sequence 10, Application US/08827223A

Sequence 10, Application US/08827223A

APPLICANT: Sej-12awa, Nobufusa

APPLICANT: Colikawa, Kimihisa

APPLICANT: Iclikawa, Kimihisa

APPLICANT: Iclikawa, Shin

TILE OF INVEITION: ANTI-FES RECOMBINANT ANTIBODIES AND DNA THEREFOR

FILE REFERENCI: 970093/HG

CURRENT APPLICATION NUMBER: US/08/827,223A

CURRENT FILIN: DATE: 1998-07-23

BEARLIER FELIN: DATE: 1996-04-01
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COMPUTER: TROABLE FORM:
MEDIUM TYP?: Floppy disk
COMPUTER: IP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: BAR-1997
CLASSIFICATION NUMBER: US/08/827,223
FILING DATE: JP Hei 8-78570
FILING DATE: JOI-APR-1997
CLASSIFICATION NUMBER: JP Hei 8-78570
FILING DATE: 01-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Goolman, Herbert
REGISTRATION NUMBER: 17081
TELECOMMUNICATION NUMBER: 17081
TELECOMMUNICATION NUMBER: 17081
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-319-4900
TELEPROXE
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Best Local Similarity 78.0's
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Length 238:
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77.1%; Score 535.5; DB 14; Length
Best Local Similarity 78.0%; Pred. No. 4.2e-45;
Matches 103; Conservative 10; Mismatches 18; Indels
                                                              18; Indels
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APPLICANT: HATUYAMMA, TOhru
APPLICANT: TAKAHASHI, TOhru
APPLICANT: NAKAHASHI, TOhru
APPLICANT: VONCHARA: KAONI
APPLICANT: VONCHARA: Shin
TITLE OF INVENTION: HUMANIZED ANTI-HUMAN FAS ANTIBODY
TITLE REPERENCE: 980125/MG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT PELING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP HEI 9-67938
SARLIER APPLICATION NUMBER: JP 703-21
NUMBER OF SEQ ID NOS: 189
SORTWARE: PATENTING DATE: 1997-03-21
STORTWARE: PATENTING NOWE: 189
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SORTWARE: PATENTING NOWE: 189
        DB 12;
        Score 535.5; DB 1; Pred. No. 4.2e-45; 10; Mismatches 18
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APPLICANT: UNO, Shinsuke
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APPLICANT: OH-EDA, Masayoshi

Search completed: April 13, 2001, 17:37:49 Job time: 166 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-129-930B-95

US-08-129-930B-11

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US-08-129-930B-11

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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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28 481 69.2 238 2 US-08-392-3884-21 39 481 69.2 238 2 US-08-926-789-12 31 481 69.2 238 3 US-09-166-093-21 32 481 69.2 238 3 US-09-166-093-21 34 481 69.2 238 3 US-09-166-094-21 34 481 69.2 238 3 US-09-166-094-21 35 481 69.2 238 4 US-09-166-094-21 36 481 69.2 238 4 US-09-166-094-11 37 481 69.2 240 3 US-09-166-094-11 38 481 69.2 240 3 US-09-166-094-11 39 481 69.2 240 3 US-09-166-094-11 481 69.2 240 3 US-09-166-094-11 481 69.2 240 3 US-09-166-094-11 481 69.2 240 3 US-09-166-094-11 481 69.2 250 3 US-09-166-094-15 42 481 69.2 250 3 US-09-166-094-15 43 481 69.2 250 3 US-09-166-094-15 44 481 69.2 250 3 US-09-166-094-15 45 481 69.2 250 3 US-09-166-094-15 46 16 69.2 250 3 US-09-166-094-15 47 481 69.2 250 3 US-09-166-094-15 48 16 69.2 250 3 US-09-166-094-15 49 481 69.2 250 3 US-09-166-094-15 40 0015662 41 481 69.2 250 3 US-09-166-094-15 42 481 69.2 250 3 US-09-166-094-15 43 481 69.2 250 3 US-09-166-094-15 44 481 69.2 250 3 US-09-166-094-15 45 481 69.2 250 3 US-09-166-094-15 46 481 69.2 250 3 US-09-166-094-15 47 TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS NUMBER OF SEQUENCES: 70 COUNTEY: US-00-00-00-00-00-00-00-00-00-00-00-00-00	### Score 558.5; DB 3; ###################################
28 481 69.2 39 481 69.2 31 481 69.2 31 481 69.2 33 481 69.2 34 481 69.2 35 481 69.2 36 481 69.2 37 481 69.2 38 481 69.2 40 481 69.2 41 481 69.2 42 481 69.2 43 481 69.2 44 481 69.2 45 481 69.2 47 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69.2 481 69	LENGTH: LANGTH: LENGTH: 131 amil TYPE: amino aci STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDENESS: STRANDEN
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1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60

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US-09-192-545-4
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               US-08-591-196-2
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                                                                       60 YLOKPGQS PKILIIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSGSTHVP 119
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                                                                                                                                                                                                                                                                                     GENERAL INFORM.TION:
APPLICANT: (hatterjee, Malaya
APPLICANT: (hotterjee, Malaya
APPLICANT: (hotterjee, Sunil K.
APPLICANT: (hotterjee, Sunil K.
TITLE OF INV;NTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INV;NTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SE(USENESS: 66
CORRESPONDENCE ADDRESS:
Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYP.: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
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Pred. No. 1.5e-46;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGE TT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/JOCKET NUMBER: 30414-20002.21
TELECOMMULICATION INFORMATION:
TELEPAN: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER STREET: 7:5 PAGE MILL ROAD CITY: PALG ALTO STATE: CA STATE: CA COUNTRY: 1/5A ZIP: 9430:1018
                                                                                                                                                                                                                                                     Sequence 2, Application US/08752844 Patent No. 5935£21
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79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YTFGGGIKLEIK 132
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Matches 105; Conserv
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US-08-752-844-2
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Sequent No. 611804

; Sequent No. 611804

; GENERAL INFORMATION:

; APPLICANT: Karasauyama, Hajime

APPLICANT: Taya, Choji

; APPLICANT: Taya, Choji

; APPLICANT: Matsucka, Kunie

; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use

; FILE REFERENCE: 799P79570

; CURRENT APPLICATION NUMBER: US/09/192.545
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APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No. 1.5e-46;
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Sequence 2, Application US/08591196; Patent No. 5977316
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TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acids
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79.5%;
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Best Local Similarity 79.59
Matches 105; Conservative
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                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                       94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                   USA
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co. Lolbner
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSPER: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAIM M
REGISTRATION NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR EQUIPMENTICS:
LENGTH: 131 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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120 FTFGSGTKLEIK 131
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                                                                                                                                                                                                                                                                 Query Match 78.6%; Score 546.5; DB 4; Length 238; Best Local Similarity 78.0%; Pred. No. 1e-45; Matches 103; Conservative 11; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                                                                          ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Sequence 5, Application US/08053171

Sequence 5, Application US/08053171

Sequence 5, Application US/08053171

SERVERAL INFORMATION:

APPLICANT: Co, Loibner

TITLE OF INVENTION: Antibody Derivatives

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

78.2%; Score 543.5; DB 1
Best Local Similarity 78.0%; Pred. No. 9.6e-46;
Matches 103; Conservative 11; Mismatches 17
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: JP HEI 9-313989
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.0
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11823-54-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION UNDRER: 30,23
REFERENCE/DOCKET UNDRER: 11823
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-053-171-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 LTFGAGTKLELK 131
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1 MKLPVRILULLEWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROBINSON, MARTYN K
APPLICANT: BRIGHT, SUSAN M
TITLE OF INVENTION: HUMANIZED CHIMERIC ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Ave. NW Suite 300
STREET: 1225 Connecticut Ave. NW Suite 300
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NOMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30.353
REGISTRATION NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application PC/TUS9102946; GENERAL INFORMATION:
                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 466-0800
TELEPAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROTHLEIN, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 173 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAIR, JOHN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.33
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein PCT-US91-02942-3
                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LTFGGGTKLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                      FILING DATE: 19
CLASSIFICATION:
                                                                               20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US91-02946-3
                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Óγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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Sequence 3. Application:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ATHWAL, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF IN'ENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SIQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                   APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
TITLE OF INVINITON: Analogue Peptides with Broad
TITLE OF INVINITON: Carcinome Specificity, and Kit and
TITLE OF INVINITON: Diagnostic Vaccination and
TITLE OF INVINITON: Therapeutic Methods
NUMBER OF SEVUENCES: 96
CORRESPONDEN'S BADRESS:
ADDRESSE: V. AMZEL & ASSOC.
STREET: 2 155 No. 5804187th Broadway, Suite 201
CITY: Mellut Greek
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/129,930B
FILING DATE: September 30, 1993
ATTONEY/AGENT TATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 537.5; DB 1
Pred. No. 3.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                 APPLICANT: (leriani Dr., Fernando J.R. APPLICANT: (leriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNET AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERCE/DOCKET-NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
          Sequence 95, Application US/08129930B Patent No. 5804.87 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                COMPOTER REA SABLE FORM:
MEDIUM TYP3: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: n.a.
INFORMATION FCR SEQ ID NO: 95:
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Best Local Similarity 77.3%;
Matches 102; Conservative I.
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYFE: peptide US-08-129-930B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 YTFGGG5KLEIK 131
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PCT-US91-02942-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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LENGTH
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BENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Go Couto, Fernando J.R.
APPLICANT: Peterson Dr., Borry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
TITLE OF INVENTION: B.
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREFT: A44 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 75.9%; Score 527.5; DB 5; Length 173; Best Local Similarity 77.3%; Pred. No. 4.7e-44; Matches 102; Conservative 10; Mismatches 19; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATES SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
              FILING DATE: 19910429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0576600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 aminto acids
TYPE: AMINO ACID
      PCT/US91/02946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Anzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (510) 748-6688
                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02946-3
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 444 South
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                           Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence II. Application US/08129930B
Fatent No. 5804187
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ceriani Dr., Fernando J.R.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Gaurdo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: AMZE1 Ph.D., VIVIANA
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                    Ouery Match 74.7%; Score 519.5; DB 1; Best Local Similarity 77.3%; Pred. No. 2e-43; Matches 102; Conservative 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: n.a.
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 131 amino acids
amino acid
                                                                                                           MOLECULE TYPE: peptide US-07-977-696C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
US-08-129-930B-11
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US-08-129-930B-11
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RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
                                                                                                                                                              5,
                                                      Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                 Score 513; DB 1;
Pred. No. 8.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/08483389
Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, M.
                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING. DATE: 05-JUN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 05-MAY-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 20-MAY-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 20-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SUL, YOUNGER: DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SUL, YOUNGER: DATE: 27-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27866/32760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-41,337
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                        73.8%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 127 amino acids
amino acid
                                                        Query Match
Best Local Similarity 78.1;
Matches 100; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                    125 GGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                 120 GGTKLEIK 127
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TOPOLOGY:
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US-08-483-389-45
US-08-482-882-45
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                                                                                   1 MKLPVRLIVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                 Gaps
                                               1;
    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6100 Sears Tower, 233 S. Wacker Drive CITY: Chiago STATE: Illinois GOUNTRY: ISA
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/08482882
Patent No. 5773:18
GENERAL INFORMATION:
GAPPLICANT: 'Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDEN'E ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTOUR NEW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONTRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: O7-JUN 1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/286,754
APPLICATION NUMBER: US 08/102,852
Query Match
74.7%; Score 519.5; DB 1;
Best Local Similarity 77.3%; Pred. No. 2e-43;
Matches 102; (onservative 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PELLING DATE: 05-NGG-1993
PRIOR APPLICATION DATE:
APPLICATION DATE:
SPELING DATE: 22-JAN-1993
PRIOR APPLICATION DATE:
TELING DATE: 22-JAN-1993
PRIOR APPLICATION DATE:
APPLICATION DATE: 05-UNN-1992
PRIOR APPLICATION DATE: 05-UNN-1992
PRIOR APPLICATION DATE: 105-UNN-1992
PRIOR APPLICATION DATE: 105-MAY-1992
PRIOR APPLICATION DATE: 105-MAY-1992
ATTORNEY ON NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY AGENT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISTRATION NUMBER: 15,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE, DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 2:-3856
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 amino acids
no acid
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COMPUTER REA JABLE FORM:
MEDIUM TYP 3: Floppy
                                                                                                                                                                                                                                                                    121 YTFGGGTELEIK 132
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17; Indels

Length 127;

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60 GQSPQLLIYKVSNRFSGVPDRFGSGSGSGTDFTLKLSRVEAEDLGVYFCSQSTHVPYTFG 119
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                                                                                                                                                                                                                                                                                                                                               6 RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerstein, Murray & Borun
S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/26,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/009,266
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1993
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-AWY-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-AWY-1992
APPLICATION NUMBER: 33.02
REFERENCE/DOCKET NUMBER: 32.178
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  73.8%; Score 513; DB 2; 78.1%; Pred. No. 8.3e-43; tive 9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-473-503-45
; Sequence 45, Application US/08473503
; Patent No. 5869262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233 CITY: Chicago STATE: Illinois
                  SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-113D-45
                                                                                                                                                                                                                Query Match
Best Local Similarity 78.19
Matches 100; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                              Gaps
                                                                                                                                                                                             6 RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chloago STATE: 1111nois COUNTRY: United States of America LE: 6606-6402 CORPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,113D
                                                                                                        Score 513; DB 2; Length 127;
Pred. No. 8.3e-43;
9; Mismatches 17; Indels
                                                                                                                                                            17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-487-113D-45
; Sequence 45, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
; TTLE OF INVENTION:
ITLE OF INVENTION:
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS;
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-AM-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,689
FILING DATE: 27-AM-1992
ATTORNEY/AGGIT INFORMATION:
NAME: NO. 5837872And. Greta F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: NO. 587822and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
                                                                                                  73.8%;
78.1%;
                                                                                           Query Match 73.89
Best Local Similarity 78.19
Matches 100; Conservative
          protein
                                                                                                                                                                                                                                                                                                                                                                                              125 GGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                             120 GGTKLEIK 127
: MOLECULE TYPE:
US-08-483-389-45
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Search completed: April 13, 2001, 15:36:11 Job time: 129 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Search time 32.39 Seconds (without alignments) 297.043 Million cell updates/sec April 13, 2001, 15:36:46 Run on:

US-08-700-737-15 Title: Perfect score:

MGWSCIILFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140 Sequence:

Scoring table:

198801 seqs, 68722935 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

198801 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_67:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	script	ere atedo wheel of	1 1 1 1	heavy chain	d heavy chain	heavy chain	g heavy chain pr	d heavy chain	g heavy chain V	vvedd p	a heavy chain	a heavy chain	heavy chain	heavy	a heavy chain	n heavy chain	n heavy chain	_	heavy	a heavy chain	heavy chain	heavy	Theavy chain	Theavy chain	ene VH10	מילי אאפסר	ntibody gab To	ncirody rap of		g heavy chain pr
SUMMARIES	ID	E32513	MHMS18	JL0076	A30577	A27472	HVMST7	HVMS02	B47159	G2MS43	PL0208	E29380	F29380	JL0077	HVMS3	HVMS61	B22769	PH1482	HVMSG7	PS0024	S41394	HVMS23	MHMSB4	S21810	184704	PH1489	\$53751	HVMS45	A27609	A39276
	DB	7	-	7	~	~	ч	-	~	-	~	7	~	~	7	7	~	7	-	~	~	-	-	~	~	~	~	-	7	7
	Length	138	139	141	135	131	. 138	117	136	137	136	137	137	136	117	117	120	140	140	139	120	117	117	138	116	140	116	117	139	141
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	Score	603	599.5	592.5	579.5	576	559	556	555	554.5	n	551.5	2	9	543	ഗ	533.5	533		529.5		527	525	524	523	S	519.5	519	518.5	_
	Result No.	1	7	m	ಶ	ស	9	7	<b>&amp;</b>	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	58	53

Ig heavy chain v r	heavy	perb leader/1g hea Ig heavy chain v r	heavy	Iq heavy chain pre	Iq heavy chain V r	Ig heavy chain v r	Ig heavy chain v r	Id heavy chain V r	Id damma-2a chain	heavy	Ig heavy chain V r	heavy	Gamma	Ig heavy chain pre
PH1484	520646	S25175	PH1488	H32513	S20643	PH1493	PH1486	PH1498	537483	PN0444	PH1492	A36194	S31930	S04575
7	N <	* ~	~	7	~	N	~	~	7	~	~	~	7	~
140	123	120	140	137	122	135	140	140	469	150	135	140	126	140
68.3	0.89	67.9	67.5	67.3	67.0	67.0	66.8	8.99	8.99	9.99	66.4	66.4	66.4	66.1
517	514 F	514	511	509.5	202	202	206	206	505.5	504.5	503	. 503	502.5	200
30	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

Gaps .. Length 138; 79.7%; Score 603; DB 2; Length 13. 82.9%; Pred. No. 2.6e-44; 1.1ve 7; Mismatches 15; Indels Best Local Similarity 82.9 Matches 116; Conservative Query Match

ä

1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60 δ g

61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120 δy

61 GGGLEWIGNIYPGSSSTNYNEKFKSKATLTVDTSSSTAYMQLSSLTSDDSAVYYCARRLY 120 qq

121 DGWDYAIDYWGQGTSVTVSS 140 ò

QQ

RESULT MHMS18

Ig heavy chain precursor V region (B1-8) - mouse
N:Contains: 1g heavy chain precursor V region 186-2
S.Species: Mus musculus (house mouse)
C.Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 22-Jun-1999
C.Accession: A50809; B90809; A22769; A02034; A02036
R.Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981
A.Title: Heavy chain variable region contribution to the NP(b) family of antibodies:

A; Accession: A90809

A; Molecule type: DNA A; Residues: 1-139 <B18>

A;Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115 A;Accession: B90809

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61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAREGP 120
       GOGLEWIGEIDPSESNINYNOKFKGKATLIVDISSSTAYMQLSSLISEDSAVYXCARGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GYDGWDYAIDYWGQGTSVTVSS 140
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82.8%;
                                                                                                              121 DGWDYAIDYWGQGTSVTVSS 140
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78.9%;
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-135 <KOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A30577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;69-85/Region: VF;118-125/Region:
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C; Species: Mus musculus (house mouse)
C; Accession: JL00'6
C; Accession: JL00'6
R; Kaartinen, M.; Accea-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A; Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea A; Accession: JL00'6
A, Molecule type: JRNA
A; Residues: 1-141 < KAAA
A; Residues: 1-141 < KAAAA
A; Molecule type: DNA
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Mote: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt A; Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
B; Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
BEMBO J. 1, 635-646, 1982
A; Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A; Reference number: A90971; MUID: 84236026
A; Accession: A22769
A; Molecule type: Frotein
A; Residues: 20-135 < DIL>
A; Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch variant mu chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                           A) Introns: 16/1
C; Superfamily: inmunoglobulin V region; immunoglobulin homology
C; Superfamily: inmunoglobulin predicted <SIG>
C; Keywords: heterctetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
F; 118-124/Region: D segment
F; 118-124/Region: J segment (JH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GRGLEWIK;RIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120
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Ig heavy chain procursor V region (anti-phenyloxazolone, 18C10)
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Pred. No. 2.1e-43;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 599.5; DB 1
Pred. No. 5.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
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80.0%;
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80.7%;
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Best Local Similarity 80.7'
Matches 113; (onservative
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F;136-141/Region: C
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Best Local
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A27472

19 heavy chain precursor V region (IE9) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996

C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996

C;Accession: A27472

R;Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.

Gene 54, 33-40, 1987

A;Title: Expression of mouse::human immunoglobulin heavy-chain cDNA in lymphoid cells

A;Reference number: A27472; MUID:87277430
Igheavy chain precursor V region (MRL10) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996

C;Accession: A30577

R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th

J. Exp. Med. 161, 805-815, 1985

A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;20-131/Product: ig heavy chain V region IE9 #status predicted <MAT> F;34-117/Domain: immunoglobulin homology <IMM> F;69-85/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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A; Residues: 1-131 <LIU>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 5-54/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin homology
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Pred. No. 4.7e-42;
4; Mismatches 15;
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Pred. No. 2.5e-42;
8; Mismatches 13;
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complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                A)cross-references: GB:M37621
C;Superfamily: immunoglobulin V region; immunoç
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region, anti-carcinoembryonic maid T84.66 antigen monoclonal anti-id CiSpecies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 12-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C; Accession: B47159
R; Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J; Biol. Chem. 268, 14138-14145, 1993
A; Title: Molecular characterization of a cloned idiotypic cascade containing a networ A; Reference number: A47159; MUID: 93300804
A; Reference number: A47159
A; Residues: preliminary
A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
C; Superimental source: hybridoma 6G6.C4
A; Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBIP:134422)
C; Superimenty: immunoglobulin homology cIMM>
F; 34-117/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-137 <BOT>
A;Cross-references: GB:J00539; NID:g195118; PIDN:AAA38172.1; PID:g195119
A;Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGGLEWIGRIDPYDSVTHYNQKFRDKAILTVDKSSSTAFWQLSSLTSEDSAVYYCTRMDY 120
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C; Keywords: heterotetramer; immunoglobulin
F;1.19.7Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (102) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                      Score 556; DB 1; Le
Pred, No. 2.1e-40;
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                                                                                                                                                          73.48;
89.78;
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                                                                                                                                                                                                           Matches 104; Conservative
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Matches 106, Conservative
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                                                                                                                                                          Query Match
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A.Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an A; Reference number: A02033; MUID:84248078
A; Accession: A02033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: A02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change_23-Aug-1996
Cispecies 102-Apr-1982 #sequence_revision 02-Apr-1982 #text_change_23-Aug-1996
Ribothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981
A.Title: Heavy chain variable region contribution to the NP(b) family of antibodies: A.Reference number: A90809; MUID:81234548
A.Reference number: A90809; MUID:81234548
A.Reference number: A90809; MUID:81234548
A.Residues: 1-117 <BOT>
A.Residues: 1-117 <BOT>
A.Residues: 1-117 <BOT>
A.Rote: the germline gene, cloned from the germline gene
A.Rote: the germline gene, cloned from a library of strain C57BL/6 DNA, is one of a set (NPb antibodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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A. Residues: 1-138 <GIL>
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Seywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig haavy chain V region (TEPC 1017) #status predicted <MAT>
F:21-117/Region: V segment
F:34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain precursor V region (TEPC 1017) - mouse C;Species: Mus musculus (house mouse) C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997 C;Accession: A02033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                    Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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77; Conservative
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                                                                                                                                                                                                                            DGWDYAIDYWGQGT 134
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Best Local Simi
Matches 107;
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A; Residues: 1-137 <CHE>
A; Cross-references: GB:M17164; GB:J02815; NID:g195411; PIDN:AAA38295.1; PID:g195412
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (Labortalise)
C;Species: Mus musculus (Labortalise)
C;Accession: F29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J; Biol. Chem. 262, 113599-13583, 1987
A;Fitle: Nucleotide and translated amino acid sequences of cDNA coding for the A;Reference number: A92612; MUID:88007582
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                                                                            cDNA coding
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Pred. No. 5.8e-40;
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       A.; Ratcliffe,
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R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; F
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino &
A;Reference number: A92612; MUID:88007582
A;Accession: E29380
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77.9%;
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Best Local Similarity 75.09
Matches 105; Conservative
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A; Residues: 1-137 <CHE>
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C;Species: Mus musculus (house mouse)
C;Species: Puble; S #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C;Accession: PLO2(8
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
MOI. Immunol. 27, 429-433, 1990
A;Title: Nucleotice sequence of the VH, VL regions of an anti-idiotopic antibody reactin A;Reference number: PLO207; MUID:90309764
A;Reference number: PLO207; MUID:90309764
A;Reference number: PLO207; MUID:90309764
A;Reference number: PLO207; MUID:90309764
A;Reference number: PLO207; MUID:90309764
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology cimpoler F;30-54/Region: ccmplementarity-determining 1
F;60-85/Region: ccmplementarity-determining 3
F;118-112/Region: Complementarity-determining 3
F;118-112/Region: D region
F;122-136/Region: U region
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C;Species: Mus mus culus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: E29380
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                                                                                                                                                                                                                                                                                                                                  Length 137;
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              C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                            F.1-19/Domain: Signal Sequence #status predicted <SIG>
F.20-137/Product: Ig heavy chain V region (S43) #status
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-122/Region: D segment (JH2)
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                                                                                                                                                                                                                                                                                                                              Score 554.5; DB 1
Pred. No. 3.3e-40;
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                                                  C; Keywords: heterctetramer; immunoglobulin
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74.1%;
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106; Conserv
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Matches 106;
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Best Local Similarity
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C; Superfamily:
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               A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973
A;Accession: JL0077
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R; Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Csell 24, 625-637, 1981
A:Title: Heavy Chain variable region contribution to the NP(b) family of antibodies: som
A; Reference number: A90809; MUID: 81234548
A; Accession: A02031
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C;Species: Mus musculus (house mouse)
C;Date: 02-Apr.1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-117 <BOT>
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was determined from a library of strain C57BL/6 DNA, is in (NPb antibodies)
C; Genetics:
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: signal sequence #status predicted <SIG>
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-117/Product: Ig heavy chain V region (3) #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                            A; Residues: 1-136 <RAA>
A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Note: the authors translated the codon AGC for residue 114 as Arg
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
E; 1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F; 1-15/Pomain: signal sequence (fragment) #status predicted <SIG>
F; 17-136/Product: Ig heavy chain #status predicted <MAT>
F; 17-51/Region: complementarity-determining 1
F; 18-136/Region: Omplementarity-determining 2
F; 118-136/Region: J2 segment
F; 131-136/Region: C
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Pred. No. 2.6e-39;
5; Mismatches 9;
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Pred. No. 1.5e-39;
7; Mismatches 17;
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88.0%;
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Best Local Similarity 77.4%;
Matches 106; Conservative
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Matches 103; Conservative
                                                                                                  A; Molecule type: mRNA
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If heavy chain precursor V region (186-1) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 31-Mar-1989 #text_change 23-Aug-1996 C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 23-Aug-1996 C; Accession: D90809; Accession: B00809; MulD: Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981 A: Title: Heavy chain variable region contribution to the NP(b) family of antibodies: A; Reference number: A90809; MulD: 81234548
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-117 <BOT>
A; Note: the sequence was determined from the germline gene
A; Note: the 186-1 germline gene, cloned from a library of strain C57BL/6 DNA, belongs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence fistatus predicted <SIG>
F:20-117/Product: Ig heavy chain V region (186-1) #status predicted <MAT>
F:30-117/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.3e-39;
5; Mismatches 13
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                                                                                                           1 MGWSCIILFLVSTATSVHSQ........DGWDYAIDYWGQGTSVTVSS 140
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            Compugen Ltd
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics. The European Bioinformatics in the European Bioinformatics as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P06326 homo sapien
P01742 homo sapien
P01768 homo sapien
P01801 mus musculu
P01772 homo sapien
P01799 mus musculu
P01790 homo sapien
P01806 mus musculu
P01760 homo sapien
P01794 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- MISCELLANEOÙS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
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MEDLINE-81234548; Pubmed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION B1-8/186-2.
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Pred. No. 2.4e-51;
7; Mismatches 19; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          -1707_MOUSE STANDARD; PRT; 139 AA. P01751; P01752; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1G HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
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JH2 SEGMENT
                          HV1A_HUMAN
HV3G_HUMAN
HV3X_HUMAN
HV3X_HUMAN
HV3K_HUMAN
HV1A_HUMAN
HV1A_HUMAN
                                                                                                                                                                                                            HV35_MOUSE
HV27_MOUSE
HV25_MOUSE
       HV1F_HUMAN
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Best Local Similarity 80.7%;
Matches 113; Conservative 7
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SEQUENCE
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HV07_MOUSE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mushinski J.F.,
                      GQGLEWICEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY
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  MGWSCIII.FLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tucker P.W.;
"Illegitimate recombination generates a class switch from C mu delta in an 19D-secreting plasmacytoma.";
Proc. Natl. ?cad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
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COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=8424£078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                             23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                           138 AA
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PIR; A0203; HVMs...
InterPro; IPF003006; -.
Pfam; PP00047; ig; 1.
Immunoglobulin V region; Signal.
1 20 IG H7
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HV06_MOUSE
ID HV06_MOUSE STANDARD; I
AC PO1750;
DT 21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                          121 YGSSY-FIYWGQGTTLTVSS 139
                                                                                                                                                      DGWDYAIL YWGQGTSVTVSS 140
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138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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P03980;
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HV48_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                  antibodies: somatic mutation evident in a gamma 2a variable region."; cell. 24:625-637(181).
-1- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
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                                                                                                                                                                                                                                      MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies: somatic mutation evident in a gamma 2a variable region." cell 24:625-837(1981).
-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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0
                                                                                                                                                                                                                                                                                                              contribution to the NPb family of
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                        Baltimore D.;
"Heavy chain variable region
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89.78;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6;
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117
117 A
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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-1. MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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MEDLINE-81234548; Pubmed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING 2.
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v 74.1%; Pred. No. 5...
9; Mismatches
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 3 PRECURSOR.
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Matches 106; Conservative
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137 AA;
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AC P01749;
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-1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                 COMPLEMENTARITY - DETERMINING 1.
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                                                                             IG HEAVY CHAIN V REGION 3.
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88.0%; Pred. No. 5.9e-46;
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Pred. No. 2.2e-45;
5; Mismatches 13;
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01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1999 (Rel. 138, Last annotation update)
IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
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MEDLINE=81234548; PubMed=6788376;
       EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3. InterPro: IPR003006; -. PFam; PF00047; ig; 1. Immunoglobulin V region; Signal. SIGNAL 1 19
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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84.6%;
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Best Local Similarity 88.0
Matches 103; Conservative
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Best Local Similarity 84.6
Matches '99; Conservative
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ID HV09_MOUSE
AC P01753; P11271;
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Baltimore D.;
"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                          Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V REGION 23 PRECURSOR.
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83.8%;
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                            1 MGWSCII. FLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYWQLHSLTSEDSAVYYCAR 117
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
BUS MUSCALUS (Mouse).
Mammalia, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eu.heria; Rodentia; Sciurognathi; Muridae; Murinae; Muscull_TaxID-1)090;
                                                        1 MGWSCIM FLAATATGVHSOVOLQOPGAELVKPGASVKLSCKASGYTFTSVWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.3%; Score 532; DB 1; Length 140; 72.1%; Pred. No. 8.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Somatic mutition in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;
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21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Similarity
Matches 101; Conserv
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ID HV04_MOUSE
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                                                                       ö
                                                                                                                                              1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                               61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                  61 GOGLEWIGNINPGNGGTNYNEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYCAR 117
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Length 117;
   Score 527; DB 1;
Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
Mus musculus (Mouse).
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                                     Pred. No. 2.16
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HV15_MOUSE
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-I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION VH558 B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.4%; Score 525; DB 1; Length 117; 82.9%; Pred. No. 3.2e-44; Live 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK 2
                             email to license@isb-sib.ch)
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InterPro; IPR003006; -- Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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Matches 9
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                                                                                                                                                                                                                                                   1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S. Blattner F.R.,
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                                                                                                                                                                                                                                                                                                                                                                          61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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8
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 519; DB 1; Length 11
Pred. No. 1.2e-43;
5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION BCL1
                                                                                         MW; D37DE8A3F543E996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
                                               FRAMEWORK 3.
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MEDLINE-82222262; PubMed-6806821;
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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82.9%;
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Matches 97; Conservative
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MEDLINE-83131846; PubMed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rotistein A.:
"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Bur. J. Imm.nol. 12:1023-1033(1982).
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=8418:519; PubMed=6201362;
Didrop R., Novens J., Siekevitz M., Beyreuther K., Rajewsky K.;
A V region (leterminant (idiotope) expressed at high frequency in B lymphocytes: as encoded by a large set of antibody structural genes.";
EMBO J. 3:51:-523(1984).
PIR; A02037__MHMS15.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
16 HEAVY CHAIN V REGION 36-65.

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Actaoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuscallaraxID=10090;
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Sciurognathi; Muridae; Murinae; Mus.
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75.2%; Pred. No. 8.4e-40;
iive 7; Mismatches 22
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 15.3.
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Eukaryota; Mctazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Best Local Simi arity 75.2
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Biochemistry 21:5415-5424(1982).
-!- MISCELLANDOUS: THE ESQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
-!- PROTEEN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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-i- MISCELLANDOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE 5
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MEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley Hood L.E.;
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Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Glycoprotein.
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DT 21-UUL-1986 (Rel. 01, Created)

DT 21-UUL-1986 (Rel. 01, Last sequence update)

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DE GARATYOLE; MEELZOA; Chordata; Craniata; Vertebrata; Euteleostomi;

OC BUARTYOLE; MEELZOA; Chordata; Confordata; Cohen J., Glvol D.;

RN MEDLINE-81053741; Pubmed-6253904;

RN MEDLINE-81053741; Pubmed-6253904;

RN MEDLINE-81053741; Pubmed-6253904;

RN AZAKUT R., Cohen J., Glvol D.;

RN T. "Cloning and sequence of the coha corresponding to the variable RN Tregion of immunoglobulin heavy chain MPC11.";

RN I2]

RN RT SAULT R., Cohen J., Glvol D.;

RN I2]

RN AZAKUT R., Cohen J., Glvol D.;

RN LOLEIC Acids Res. 8:4839-4840(1980).

FROM A MYELOMA THAT SECRETES IGG2B.

RN AZAKUT R., Cohen J., Glvol D.;

FROM A MYELOMA THAT SECRETES IGG2B.

RN FERP ROOUGH; 19:1

RN Immunoglobulin V region.

FR Immunoglobulin V region.

FR INON_TER I21 AA: 13135 MW; 227AEF3EC56EDOBF CRC64;
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Search completed: April 13, 2001, 15:40:19 Job time: 272 sec

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Query Match 59.0%; Score 447; DB 1; Length 121; Best Local Similarity 69.4%; Pred. No. 1.2e-36; Matches 84; Conservative 12; Mismatches 25; Indels

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Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.......DGWDYAIDYWGQGTSVTVSS 140

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
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| Sp\_archea:\*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Odilo mus musculu	0 0				Obside mins muscuil	Obiilos bano arrita			OAJIB3 mus musculu	Q9y298 homo sapien	O9ul95 homo sapien	Q9j185 mus musculu	095978 homo sapien	Q9u189 homo sapien	Ogavfo mus musculu	Ogulda homo ganion			
SUMMARIES		QI	090XE9	093177	09JL81	090XF0	0921C4	09JL75	0921C6	0901.92	100 TILL 94	00 11 03	00000	0011290	090195	090185	97850	687060	O9QYF0	Q9UL93	090190	Q9Y509	
	Query	Length DB	117 11	110 11	114 11	117 11	118 11	109 11	117 11	124 4	119 4	110 11	150	1001	120	103	, CT	110 4	TT 867	116 4	113 4	147 4	
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## ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mammaliai: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mammaliai: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus SEQUENCE FROM N.A.  Langer A., Specht C., Koalsch E.;  SEQUENCE FROM N.A.  Clemens A., Rademaekers A., Specht C., Koalsch E.;  SEDULAITER (DEC-1997) to the EMBL/GenBank/DDBJ databases.  EMBL; AJZ25174; CAB65237.1;  NON_TER 117  INNERPRO; IRRO/A 117  NON_TER 117  NON_TER 117  NON_TER 117  SEQUENCE 117 AA; 13000 MW; CDDEZAF84D499734 CRC64;  SEQUENCE 117 AA; 13000 MW; CDDEZAF84D499734 CRC64;  SEQUENCE 117 AA; 13000 MW; CDDEZAF84D499734 CRC64;  SEQUENCE 117 AA; 13000 MW; CDDEZAF84D499734 CRC64;  SEQUENCE 117 AA; 11000 MM; CDDEZAF84D499734 CRC64;  SEQUENCE 117 AA; 11000 MM; CDD	S A., o the 37.1; 2.5%; 2.5%; 1.11! VKLSCK ITAYMQLL ITAYMQLL ITAYMQLL ITAYMQLL ITAYMQLL
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characteri.ation of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucksamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APZ060423.1; -.
NON TER 1 1
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                                                                                                                                                            STRAIN=DBA/2.

Malkiel S., Jao L., Cunningham M.W., Diamond B.;

"characterization of cross-reactive monoclonal anti-myosin/anti-n-
"characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-gluco;amine antibodies from mice with autoimmune myocarditis.";

Submitted (NY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF206019; AAF69237.1;
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                                                                                                                                                                                                                                                                                                                                         30 LVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKATL 89
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Netzoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthezia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                01-0CT-2000 TrEMBLrel. 15, Created)
01-0CT-2000 TrEMBLrel. 15, Last sequence update)
01-0CT-2000 TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN :MMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                  Mus musculus (Mouse),
Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eucheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LTVDKS3STAYMQLSSPTSEDSAVYYCARSNYYGSSLYYFDYWGQGTTLTVSS 114
                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 462.5; DB 11; Length 114;
Pred. No. 3.7e-40;
7; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                             DB 11; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                          {\tt TVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS~140}
                                                                                                                                                                                                                                                                                                                                                                                                         12829 MW; 404885FDE6BA56F8 CRC64;
                                                                                                                                                                                                                                                        12138 MW; ZEDE81FB5862C9AF CRC64;
                                                                                                                                                                                                                                                                                          61.4%; Score 464.5; DB 1.79.3%; Pred. No. 2.2e-40; iive 7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AA.
           110 AA.
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larity 77.9%;
Conservative
                                                                                                                                                                                                                                                                                                                     Conservative
          PRELIMINARY;
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Best Local Sim.larity
Matches 88; Conserv
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Matches 88; Conserv
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                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=10090;
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SEQUENCE
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SEQUENCE
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09JL81;
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              Q9JL77
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09JL77
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Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P., Matis L.M., Evans M.J., "Humanized porcine VCAM-specific monoclonal antibodies with chimeric 19G2/64 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYYCARDK----DYYFDYWGQGTTLIVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TTEWBLrel. 10, Last sequence update)
01-MAY-2000 (TTEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                        Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225171; CAB65236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13060 MW; D816AD0858A47E4C CRC64;
                                                  01-MAY-2000 (TrEMBLrel. 13, Créated)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
1MMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6%; Score 459; DB 11;
72.7%; Pred. No. 8.7e-40;
ive 11; Mismatches 18;
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117 AA
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11, Mismatches
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  PRELIMINARY;
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117 AA;
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Best Local Similarity
Matches 88; Conserv
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Length 118;

DB 11;

Score 458.5;

60.68;

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Malktel S., Lido L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206031; AAF205031; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C;
Mueller J.P., Glannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Mutals L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
1962/64 constant regions block human leukocyte binding to porcine
                                                                                80 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGWDYAIDYWGQGTSV 136
                                                                                              Gaps
                                                   Gaps
                                     QVQLQOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JL75
Q9JL75,
Q9JL75,
Q9JC7-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q921C6 PRELIMINARY; PRT; 117 AA.
0921C6 01-MX-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT)
Mus musculus (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.5%; Score 442.5; DB 11; Length 109; 76.1%; Pred. No. 3.9e-38; Live 8; Mismatches 14; Indels 5;
 9.8e-40;
ches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
 71.8%; Pred. No. 9.8e
Best Local Similarity 71.8 Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Conservative
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                 137 TVSS 140
                                                                                                                                                      TVSS 118
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SEQUENCE
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Q9JL75
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                        20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQSGPQLVRPGTSVKISCKASGYSFTSYWMHWVKQRPGQDLEWIGNIDPSDSEVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e
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                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelk
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                 4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.8%; Score 414.5; DB 4; Best Local Similarity 64.5%; Pred. No. 3.4e-35; Matches 80; Conservative 17; Mismatches 24;
                                                                                                                                                                                                                                                     57.7%; Score 437; DB 11;
11arity 70.2%; Pred. No. 1.6e-37;
Conservative 8; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                              13122 MW;
endothelial cells.";
Submitted (NOV-1996) to the
EMBL: U78799; AAD00291.1; -.
INTERPRO; IPR003006; -.
PFAM; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                 117 1
117 AA;
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Matches 85; Conserv
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SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M. Young D.C.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                    IGG VH PROTEIN PRECURSOR (FRAGMENT).
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                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12,
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Best Local Similarity 56.44
Matches 79; Conservative
                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AA;
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SIGNAL
NON_TER
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Q9Y298;
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                                                                                                                                                                                                                                                     IGG VH
                                                                                                                              RESULT 11
Q9Y298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malkiel S., .iao L., Cunningham M.W., Diamond B.;
"Characteriz.tion of cross-reactive monoclonal anti-myosin/anti-n-acetyl-gluco;annine antibodies from mice with autoimmune myocarditis.";
Submitted (NYV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARF06013; AAF6911.1; -.
NON_TER
                                       01-MAY-2000 TrEMBLrel. 13, Created)
01-MAY-2000 TrEMBLrel. 13, Last sequence update)
01-JUN-2000 TrEMBLrel. 14, Last annotation update)
MYOSIN-REACT: VE IMMUNOSLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 NQKFKGK.\TLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDG-WDYAIDYWGQGTSVTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLQQP/;AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN (MMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eu. Arazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=1)090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 110;
                                                                                                                                                                                                        Wu X., Liu B , Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                        54.7%; Score 414; DB 4; Length 119; 65.6%; Pred. No. 3.7e-35;
                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
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                                                                                                                                                                                                                                                                                                                                                             1..9 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.5%; Score 412.5; DB 1 70.5%; Pred. No. 4.7e-35;
                                                                                                                                                                                                                                                                  Clin. Immuno... Immunopathol. 87:184-192(1998).
EMBL; AF0350:0; AAD56256.1; -.
INTERPRO; IPN003006; -.
PFAM; PF0004"; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
            119 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
              PRT;
                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=9827''139; Pubmed=9614934;
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Best Local Simi.arity 65.6%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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              'RELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 AA;
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Best'Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                       fetus."
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              Q9UL94
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Q9UL94
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN WARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-98322155; PubMed-9657749; Jacquemin M.G., Vander Elst L.P.L.; Mechanism and kinetics of factor VIII inactivation: study with an ig64 monoclonal antibody derived from a hemophilia A patient with inhibitor." Blood 92:496-506(1998). EMBL; AJ224083; CAA11829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ELVKPGASVKISCKASGYTFSNSWMNWVKLRPGQGLEWIGRIYPGDGDAYNGKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                     89 LTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                         62 LTADKSSSTAYMQLSSLTSVDSAVYFCAR---SNWDVRFAYWGQGTLVTVSA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.4%; Score 404; DB 4; Length 150;
56.4%; Pred. No. 5.2e-34;
Live 17; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16031 MW; 563D164AB22802D5 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M., Bohlen H., Diehl V., Wolf J.;

*Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with example the cellularity Hodgkin's disease is associated with class somatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJO05570; CAAA06599.1;

FEME, PFO0047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGG-
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
Young D.C.;
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157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.1%; Score 356.5; DB 4;
60.3%; Pred. No. 2.8e-29;
11ve 16; Mismatches 29;
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Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035025, AAD56261.1; -.
PFAM; PF00047; ig: 1.
NON_TER 116 116
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PROTEIN PRECURSOR (FRAGMENT)
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Best Local Similarity 60.3
Matches 70; Conservative
                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 75; Conserv
                                                                                                NCBI_TaxID=9606;
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SEQUENCE
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SEQUENCE
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Q9UL89
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"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF206021; AAF69319.1:
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                          20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.0%; Score 386; DB 11; Length 109; 64.6%; Pred. No. 2.5e-32;
                                                                                                                                                                                                            Length 125;
                                                                                                                                                                                                         Query Match 51.5%; Score 390; DB 4; Length 12 Best Local Similarity 60.0%; Pred. No. 1.1e-32; Matches 75; Conservative 16; Mismatches 30; Indels
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                                                                                                                                                 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
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Last sequence update)
Last annotation update)
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            fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035019; AAD56255.1;
INTERPRO; IPR003006; -.
PFAM; PF00047; 1g; 1.
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Matches 73; Conservative 13; Mismatches
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095978;
01-MAY-1999 (TEMBLEEL 10,
01-MAY-1999 (TEMBLEEL 11,
01-MAY-2000 (TEMBLEEL 13,
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

April 13, 2001, 15:35:39; Search time 57.59 Seconds (without alignments) 138.963 Million cell updates/sec Run on:

US-08-700-737-15 757 1 MGWSCIILFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140 Title: Perfect score:

Scoring table: Sequence:

390729 seqs, 57163235 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

390729

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_0401:\*

| SIDSI/gggdata/geneseq/geneseqp/AA1981.DAT:\*
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| SIDSI/gggdata/geneseq/geneseqp/AA1992.DAT:\*
| SIDSI/gggdata/geneseq/geneseqp/AA1992.DAT:\*
| SIDSI/gggdata/geneseq/geneseqp/AA1993.DAT:\*
| SIDSI/gggdata/geneseq/geneseqp/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. the number of Pred. No.

SUMMARIES

	Description	Murine Act-1 beam	Protein sequence	Consensus protein	Heavy chain of a h	Anti-Fas Mah HFF7a	MOUSE the Control	Muring anti-Fas an	Mah 55 1 hoann cha	Single chain antic	VEASE CHAIN ALLIN	Sequence encoded b	
	ID	W53815	W53818	W53816	W53813	W83041	B14747	W90897	R76088	W24025	R27049	P70624	
	: BB	19	19	19	19	19	21	21	16	18	13	8	
Query	Length	140	137	144	180	464	464	464	464	443	140	136	
Query	Match	100.0	96.4	94.2	83.5	81.2	81.2	81.2	78.9	78.5	77.8	77.4	
	score	757	730	713	632	615	615	615	597	594.5	589	286	
Result	9	٦	~	e	4	2	φ	7	80	6	10	11	

Anti-hepatitis B h Mouse-human chimae Chimeric anti-hepa Human anti-hepatit Human anti-hepatit Human anti-hepatit		Humanised anti-Fas Humanised HFETA de Humanised anti-Fas Anti-Fas humanised Fragment of humani Humanised anti-Fas	Anti-Fas humanised Humanised anti-Fas Humanised HFP7A de Mouse NAD 2812 H C Heavy chain variab Amino acid sequenc A dimeric anti-CD2	Monoclonal antibod Murine variable re Humanised HFE7A de p64-h2 protein pro MAD Co-1 heavy cha MOUSE CO-1 heavy c Anti-DNA antibody CO-1 Heavy Chain V Anti-tobacco mosai Anti-EGFR antibody
W10584 W16340 W10239 W47510 W41054	W89535 R84554 W90933 W83037	B14779 W90929 W90935 W83038 B14775	W83036 B14776 W90926 R12233 R12355 W50218	W44177 K55215 W50936 R29009 W6213 W85061 W07436 R09425 R66758
118 119 119 119	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	21 21 21 21 21 21	2122213	19 113 113 114 116 116
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## ALIGNMENTS

Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease. Murine Act-1 heavy chain variable region. W53815 standard; Protein; 140 AA. (first entry) 14-JUL-1998 W53815; RESULT W53815 

Mus. sp.

/note= "signal peptide" 20..140 /note= "mature protein" Location/Qualifiers Peptide Protein Key

WO9806248-A2

19-FEB-1998.

97WO-US13884. 06-AUG-1997;

96us-0700737. 15-AUG-1996;

(LEUK-) LEUKOSITE INC.

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Misc-difference 6
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Saldanha J;
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W53816
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                                                                                                                          The present sequence represents the heavy chain varaible region of murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of th.s particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a light of crapha4-beta7. It can be used for inhibiting diseases such as inflammatory bowel diseases. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein sequence of murine variable heavy chain region of clone H2B#34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                            ;
                                                             Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for trecting inflammatory disease, pancreatitis, diabetes, asthma, graff versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                    Length 140;
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  Ringler DJ;
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Pred. No. 2.4e-55;
0; Mismatches 0;
  Ponath PD,
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  Newman W,
                                                                                                          Claim 27; Fig. 9; 145pp; English
                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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Matches 140; Conservative
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    SI,
                                 WPI; 1998-15:172/14.
N-PSDB; V20078.
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              Saldanha J;
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                                                                                                                                                                                                                              The present sequence represents the amino acid sequence comprising the variable region of murine Act-1 antibody determined from clone H2B#34. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The present sequence was used to construct chimeric. In the humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised for inhibit can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus protein sequence of the murine variable heavy chain region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                        integrin
diabetes,
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                                                                     Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis, asthma, graft versus host disease and sarcoidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 730; DB 19;
Pred. No. 3.9e-53;
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                                                                                                                                                                                     Example 1; Fig 2; 145pp; English
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llarity 98.5%;
Conservative
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WPI; 1998-159172/14.
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Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 AA;
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                            N-PSDB; V20089.
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by YTC'

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Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes asthma, graft versus host disease and sarcoidosis
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'note= "not specified, encoded by RTC'
                             'note* "not specified, encoded
                                                                                                                                                     131..141
/note= "framework region 4"
                                                               20..49 //note= "framework region 1"
                                                                                             5..68
'note= "framework region 2"
                                                                                                                                  region 3"
               note "encoded by ATY"
                                              /nocc
20..144
'~~te= "mature protein"
                                           'note- "signal peptide'
                                                                                                                    /nocc
86..117
`~+~= "framework r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection, isolation and diagnosis.
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                                                                                                                                                                                                                                                   Newman
                                                                                     "CDR1"
                                                                                                                 "CDR2"
                                                                                                                                      .18..130
'note= "CDR3"
                                                                                                                                                                                                                      96US-0700737
                                                                                                                                                                                                        97WO-US13884
                                                                                                           69..85
/note=
                                                                                       note-
                                                                                                                                                                                                                                   (LEUK-) LEUKOSITE INC.
                                                                                                                                                                                                                                                  Jones ST,
                                                                                                                                                                                                                                                                      WPI; 1998-159172/14.
N-PSDB; V20085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 AA;
       Misc-difference
                     Misc-difference
                                                                                                                                                                           WO9806248-A2
                                                                                                                                                                                                      06-AUG-1997;
                                                                                                                                                                                                                     15-AUG-1996;
                                                                                                                                                                                         19-FEB-1998
                                                                                                                                                                                                                                                         Saldanha J
                                                                                                                                                                                                                                                 Bendig MM,
                                    Pept1de
                                                  Protein
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The present sequence represents the concensus minion care sequence.

Comprising the variable region of murine Act-1 antibody determined from several independent mouse heavy chain variable region clones. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell achesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.

The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Variable regions were amplified from DNA encoding Act-1 using degenerate PCR primers V20079-82. The degeneracy of the PCR primers produced several different sequences, of which the present sequence is a consensus sequence. The present sequence was used to construct chimerlo, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating infilammatory diseases such asserting a filammatory diseases such asserting a filammatory be used for antiform and also be used for antiform and also be used for antiform and also be used for antiform and also be used for antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform antiform an primers The present sequence represents the consensus amino acid sequence

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                           Gaps
                         0
    DB 19; Length 144;
                         Indels
                        1;
   Score 713; DB 19
Pred. No. 1e-51;
0; Mismatches
   94.2%;
Query Match
Best Local Similarity 99.3'
Matches 133; Conservative
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The present sequence represents the heavy chain of humanised murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                           Mouse; Act-1 antibody; human alpha4-beta7 integrin; wascosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease;
IGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ringler DJ;
                                                                                                                                                                                                                                                                                      Heavy chain of a humanised murine Act-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide" 20..180 /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mature protein"
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                                                                                                                                                                                                  W53813 standard; Protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Fig 11; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel disease
                                                                                                                                                                                                                                                           (first entry)
                                                                                                 127 IDYWGQGTSVTVSS 140
                                                                                                                 Jones ST,
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N-PSDB; V20076.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                        29
                                                                                                                                                                    RESULT
W53813
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(SANY ) SANKYO CO LTD.
                 Akio S, Hid
Masahiko O,
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B14747
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                                                                                   WIGEIDP: ESNINYNQKFKGKATLIVDISSSIAYMQLSSLISEDSAVYYCARGGYDGWDY 125
                                                                                          Gaps
                                                            65
                                                   6 IILFLVS1ATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLE
                                                                                                                                                                                                                                                    apoptosis; HIPDA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; Siogrem syndiome; pernicitous anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid a:thritis; autoimmune haemolytic anaemia; myasthenia g:avis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; attrr.osclerosis; myocarditis; cardiomyopathy; glomerular niphritis; hypoplastic anaemia; hepatitis; AIDS; transplant rijection; therapy; complementarity determing region;
                                   ;
                   Length 180;
                                                                                                                                                                                                                                                monoc.onal antibody; mouse; Fas; humanised antibody;
                 83.5%; Score 632; DB 19;
85.9%; Pred. No. 5.8e-45;
live 9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                1..19
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                20..464
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Constant
                                                                                                                                                                              W83041 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "claim 9"
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                                                                                                                                                                                                                               Anti-Fas MAb HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   50..54
/label= CDR_H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69..84
/label= CDR_H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDR_H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97JP-0276064.
97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                               (first entry)
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/label= C
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                                    Matches 116; (onservative
                                                                                                                    126 AIDYWGQCTSVTVSS 140
                                                                                                                              .140
                            Similarity
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25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                    Query Match
                            Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                     99
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                                                                                                                                                              RESULT
                                                                                                                                                                       W8304.
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This is the amino acid of the heavy chain of murine anti-human Fass monoclonal antibody HFE7A. CDNA (see V70129) encoding the heavy chain was obtained from HFE7A-secreting Mybridoma (FERM BP-5828).

CRNA by RT-PCR (see V70125-26). The invention provides humanised HFE7A antibodies are capable of inducing apoptosis in abnormal cells.

CRNA pressing Fas, and of inhibiting Pas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus cuch diseases, Hashimot's disease, graft versus host disease, Slogren syndrome, pernicious anaemia, Addisease, rheumatoid calcroderma, Goodpasture syndrome, Crohn's disease, rheumatoid gravis, multiple solerosis, Basedow's disease, thrombopenia purpura and insulin dependent diabetes), allergies, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; attopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61. GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                              New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
17; Indels
Kimihisa I;
                                                                                                                                                                                                                                                                                                                                                                Reference Example 4; Page 187-188; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 615; DB 19;
Pred. No. 3.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.8e
5; Mismatches
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Jun O, ;
Hideyuki H, Hiroko Y, J
O, Nobufusa S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B14747 standard; Protein; 464 AA.
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121 ysnnwyfdvwgtgttvtvss 140
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Best Local Similarity 84.3%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                  WPI; 1998-543440/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA;
                                                                                                                                      N-PSDB; V71029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-2000
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs. Complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, the treatment or prevention of conditions such as autoimmune diseases, allowerulonephritis, aplastic anaemia (panmyalophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                                                            eventive or treating agent for the diseases caused by an abnormality the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                   Example 4; Page 67-68; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.3%;
Matches 118; Conservative
                                                                                                           98JP-0276883
                                                                          99JP-0278301
                                                                                                                                                                                                                                          Preventive or treating
                                                                                                                                                (SANY ) SANKYO CO LTD.
                                                                                                                                                                                  WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 AA;
                                                                                                                                                                                                                                                                                  anti-Fas antibody
                                                                                                                                                                                                         N-PSDB; A72108.
JP2000169393-A.
                                                                        30-SEP-1999;
                                                                                                           30-SEP-1998;
                                   20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                              61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                         1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYMMHWVKQRP 60
                                                  ;
0
Score 615; DB 21; Length 464;
Pred. No. 3.8e-43;
5; Mismatches 17; Indels
                      Indels
                                                                                                                                                                                                                                                         Murine anti-Fas antibody HFE7A heavy chain protein.
                                                                                                                                                                                           W90897 standard; Protein; 464 AA
                                                                                                                      121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                    :: | || ||:|||||
121 ysnnwyfdvwgtgttvtvss 140
                                                                                                                                                                                                                                     08-AUG-2000 (first entry)
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Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; denti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosupressive, thyrominetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatold arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;

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New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                                                                                                                 Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                 Example reference 4; Page 100-102; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.2%; Score 615; DB 21;
Best Local Similarity 84.3%; Pred. No. 3.8e-43;
Matches 118; Conservative 5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ysnnwyfdvwgtgttvtvss 140
                                                                99EP-0307711.
                                                                              98JP-0276881
                                                                                     98JP-0276882
                                                                                                                 Serizawa N, Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                     the invention.
                                                                                                   (SANY ) SANKYO CO LTD.
                                                                                                                              WPI; 2000-258930/23.
N-PSDB; A11546.
                                                                                                                                                                                                                                                                                                                                                                                                   464 AA;
                      Mus musculus.
                                                               29-SEP-1999;
                                                                              30-SEP-1998;
                                                                                     30-SEP-1998;
                                                  05-APR-2000.
                                   EP990663-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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121 ygyddamdywgggtsvtvss 140

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAD 55.1 (EC.CC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (094037) and light (094036) chains of 55.1 were isolated, and F(ab)', F(ab)'2. Fab, Fv, scFv or V-min humani.ed 55.1 constructs have been expressed in myeloma cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSCIIJFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                          Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monocolonal artibody; MAb; Immunotherapy; therapy; diagnosis; transgenic arimal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                  Antigen bind.ng structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                     Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.9%; Score 597; DB 16; 180.0%; Pred. No. 1.1e-41; ive 11; Mismatches 17;
                                                                                                                                                                 20..464
/label= Mat_protein
/note= "claim 3, page 97-98"
                                                                                                                                                                                                                                                                                     Hall SM,
                                                                                                                                                  1..19
/label= Sig_peptide
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; 'ig.15; 121pp; English.
               R76088 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                     Copley CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                               94GB-0011089.
                                                                                                                                                                                                                               94WO-GB02610.
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Best Local Similarity 80.0%
Matches 112; Conservative
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), Boot C,
Wr:ght AF;
                                                              MAb 55.1 heavy chain.
                                                                                                                                                                                                                                                                                                             WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                        (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 54 AA;
                                                                                                                                                                                                                                                                                                                     N-PSDB; Q940:17.
                                                                                                                                                                                                                                29-NOV-1994;
                                                                                                                                                                                                                                                03-JUN-1994;
                                                                                                                                                                                                                                                       03-DEC-1993;
                                               21-NOV-1995
                                                                                                                                                                                                  WO9515382-A
                                                                                                                                                                                                                 08-JUN-1995
                                                                                                                                                                                                                                                                                        Д,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                               Rose MS,
                                                                                                                                                   Peptide
                                                                                                                                                                   Protein
                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                       Blakey
                               R76088;
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                                                                                                                                             Key
RESULT
R76088
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This sequence represents a novel single chain antigen hybrid receptor (HR) and contains an extracellular domain specific for the hapten 4-hydroxy-5-iodo-3-nitrophenyl acetate (NIP) coupled to the CDB-alpha region and the transmembrane and signal-conducting intracellular parts of the CD3-zeta molecule. Such hybrid receptors comprise a receptor part notalised on the outside of the cell and specific to aparticular signal molecule and a receptor part originating from another receptor, localised on the inside of the cell and capable of setting off a signal inside the cell. The cell should also contain at least one other gene construct with a control region which can interact with the signal sent out by the hybrid receptor and thereby control expression of a transgene bound to this control region. Such cells are useful in gene therapy or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= VL_B_1-8
/note= "variable light chain region of B1-8 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= VH_B_1-8
/note= "variable heavy chain region of B1-8 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cells with hybrid receptor having extracellular and intracellular regions of different origins - useful in gene therapy and diagnosis
                                                                                                                                                                                                                     gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "single chain antigen hybrid receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bel= transmembrane_domain
                                                                                                                                                                                                                     Hybrid receptor; single chain antigen; gene signal conduction; receptor; control region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD_8-alpha_hinge
                                                                                                                                                                                                                                                                                                                                                                                                     1.19
/label= leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= (Gly,_Ser)3
/note= "linker region"
                                                                                                                                                                        Single chain antigen hybrid receptor.
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                     W24025 standard; Protein; 443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 4; 46pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mertelsmann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95DE-4045351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-DE02334
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140..154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20..444
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-319784/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T77137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9720938-A2
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kulmburg P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1997
                                                                                                                        04-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumours
                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                        W24025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                     61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                               Gaps
                                                                                                                         90
                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; complementarity determining region; framework; antigens; tumour; melanoma; carcinoma; glioma; light; heavy; variable; chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The variable heavy chain of monoclonal antibody 425 was prepd. from a synthetic cDNA sequence in which mutations had been made to the 5' and 3' ends to allow for cloning into HCMV expression vectors.
                                                                                                                                   1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human monoclonal antibodies binding to human receptors - for treatment and diagnosis of tumours, e.g. melanoma and carcinoma
                                                                     Length 443;
                                                                                               Indels
                                                                   DB 18;
                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.140
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saldanha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        Š.
                                                                                                                                                                                                                                                                                                                                                                                                 VH425 antibody cloned into pUC18.
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                                                                                                                                                                                                                                                                                                                   R27049 standard; Protein; 140
                                                                                                                                                                                                                        121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                         121 ygssy-fdywgqgttvtvss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kettleborough CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69..85
/label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50..54
/label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118..129
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-EP00480
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERE ) MERCK PATENT GMBH.
                                                                           Best Local Similarity 80.7 Matches 113; Conservative
 diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1992-331729/40.
                           443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; 028739
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9215683-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bendlg MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                          Sequence
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                               R27049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                      R27049
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Gaps
                                                                                                                                                                                                                                                                                                                   GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                      1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSVWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patentors claim a chimeric antibody molecule comprising 2 light chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonuclectides (UIGs) for use as primers or probes for cloning immunoglobulinlight or heavy chain mixes or genes. Depending on the nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific J sequence. UIG denotes universal immunoglobulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoded by anti-hepatitis B heavy chain variable region in pING2006E.
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The
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Donor splice sites were recreated in the 3' flanking regions tallow correct splicing of the variable and constant regions. 5' sequence was altered to introduce an initiation codon. The cloned antibody may be used int the prodn of reshaped or humanitsed antibodies which are less immunogenic than native antibodies and may be used to combat e.g. glioma, melanoma or carcinoma.
                                                                                                                                                                                      Length 140;
                                                                                                                                                                                   Score 589; DB 13; Length 14
Pred. No. 1.5e-41;
6; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of immunoglobulin chains and molecules DNA procedures, with chimeric antibodies etc. specific antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric antibody; Anti-cancer antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 12B; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70624 standard; protein; 136
                                                                                                                                                                                                                                                                                                                                                                                     121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86WO-US02269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85US-0793980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENETIC ENG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                 Query Match
Best Local Similarity 80.7
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-136004/19.
N-PSDB; N70967, N70968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson RR, Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ITGE-) INT GENETIC EN (ROBI/) ROBINSON R R.
                                                                                                                                  140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-0CT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8702671-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1987
                                                                                                                                   Seguence
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(XOMA ) XOMA CORP
                                                                                                                                                                                                                                                                        RESULT
W16340
                                                                                                                                                                                                                                                                                                            Db
δy
                                                                                                                                                                  qq
                                                                                                                                                                                      δ
                                                                                                                                                                                                      g
                                                                                                                                                                                                                           Qγ
                                                       ;
;
                                                                                                             61 GOGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                       1 MGWSCII), PLUSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The cDNA secuence encoding present anti-hepatitis B heavy chain variable secuence, was used in the preparation of a novel polynucledrotide molecule encoding an Ig fragment. The DNA molecule conprises 2 DNA sequences encoding 2 pectate lyase secretion signal sequences respectively linked to a DNA sequence from Ight Canain, operably linked to a single prokeryotic promoter so as to form a dicistronic transcripticn unit, provided that the Ig fragment can bind an
                                                                                                                                                                                                                                                                                          Immunoglobulin G; IgG; heavy chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunoassay; imaging; reagent; complement mediated lysis; therapy; hepatitis B virus; variable region; HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acić encoding immunoglobulin fragment - comprising
di:cistronic transcription unit with pectate lyase signal sequences
                                                         ۲,
                                     Length 136;
                                Score 586; DB 8; Length 13
Pred. No. 2.6e-41;
"..matches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson RR;
                                                                                                                                                                                                                                                                         Anti-hepatitis B heavy chain variable region.
                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu AY,
                                                                                                                                                                                                                    W10584 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 12B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lei S,
                                                                                                                                                    121 DGWDYAINYWGQGTSVTVSS 140
                                                                                                                                                              90US-0501092.
85US-0793980.
86WO-US02269.
87US-0077528.
92US-0987555.
94US-0299085.
                                     Query Match 77.4%;
Best Local Simi.arity 81.4%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                85US-0793980
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-107579/10.
N-PSDB; T36303, T36304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (XOMA ) XOMA CORP.
             AA;
            1:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1985;
27-OCT-1986;
                                                                                                                                                                                                                                                         21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                              US5595898-A.
                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Better M,
             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall R,
                                                                                                                                                                                                                                                                                                                                            Mus spp.
                                                                                                                                                                                                                                        W10584;
                                                                                                                                                                                                   RESULT 12
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                        Antibody engineering; heavy chain; light chain; chimaeric antibody; passive immunisation; diagnosis; hybridoma; hepatitis B virus; HBSAg; pING2006E; pING2012E.
antigen and is produced and secreted by an E. coli host cell when the nucleic acid molecule is expressed in the host cell.

The polynuclocided molecule is used for the production of recombinant antibodies; which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging reagents, in complement mediated lysis and for therapeutic purposes when coupled to a toxin or other therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                       Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mouse heavy chain variable region"
                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse-human chimaeric anti-hepatitis B heavy chain.
                                                                                                                                                                                                                                     Score 586; DB 18;
Pred. No. 2.6e-41;
5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= J
/note= "human J region"
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W16340 standard; Protein; 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 d-w---faywgggtlvtvss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-0501092.
85US-0793980.
86WO-US02269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88US-0142039.
92US-0870404.
94US-0235225.
                                                                                                                                                                                                                                             77.4%;
81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0077528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85US-0793980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.4
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimaeric Mus sp.;
Chimaeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                      136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1990;
01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-1988
17-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1994
                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W16340;
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us-08-700-737-15.rag

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09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USS698435-A.
                                         Better M,
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
    QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin; protein production; human; constant region; passive immunisation; toxin; serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm; antibody; Iq; heavy-chain; hepatitis; mouse; chimera.
                                                                                                                                                                                                                                                                                                                                   61 GOGLEWIGEIDPSESNTNYNOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                      A chimaeric polypeptide (W16340) comprises a mouse anti-HBsAg heavy chain variable region (derived from hybridoma ATCC CRL8017) and a human J region sequence. It is encoded by DNA sequences in plasmids pINC2006E (T70867) or pINC2012E (T70858). A complete polypeptide, comprising the mouse anti-HBsAg heavy chain variable region and human constant region, has been expressed in bacterial and transfected mouse cell hosts. Gene amplification has allowed prodn. of chimaeric heavy chain.
                                                               Secretable immunoglobulin heavy and light chain fragments - capable of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc
                                                                                                                                                                                                                                               Length 136;
                                                                                                                                                                                                                                                                  17; Indels
          Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric anti-hepatitis heavy chain from pING2006E.
                                                                                                                                                                                                                                            Score 586; DB 18;
Pred. No. 2.6e-41;
5; Mismatches 17;
                                                                                                      Example 2; Fig 12B; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               W10239 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                               s,
          Lei S,
                                                                                                                                                                                                                                                                                                                                                             121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                         77.48;
81.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85US-0793980.
86WO-US02269.
87US-0077528.
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92US-0987555.
93US-0020671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85US-07939B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0501092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1997 (first entry)
                                                                                                                                                                                                                                                              Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Homo sapiens.
Chimeric - Mus musculus.
         , Horwitz AH, Wilcox GL;
                                   1997-225473/20
                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                Sequence 136 AA;
                                              N-PSDB; T70857-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-0CT-1986;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
22-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5576195-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1990;
01-NOV-1985;
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                                                                                                                                                                                                                                            Query Match
                 Wall R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   W10239;
         Better
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                 121
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ò
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This sequence represents a fragment of the human-mouse chimeric anti-hepatitis heavy chain encoded by the gene contained within processors. PinC2006E. Thic2006E was used in the method of the invention to express the chimeric heavy chain. The method of the invention to express the chimeric heavy chain. The method of the invention is for the production of a protein in a Gram-negative bacterium. The method improves on current techniques, by using a vector including DNA encoding the pectate lysse signal sequence (see T51034), attached to the sequence encoding the protein for production. The method is especially used to make immunoglobulins (Ig), particularly those with a human constant region, suitable for passive immunosation (without risk of serum sickness or anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The ignay also be used therapeutically, optionally coupled to toxins, etc.

Alternatively the protein to be produced is the sweetener thaumatin. The presence of this signal sequence means that the protein is exported from the cytoplasm and can be recovered from the culture medium or periplasm, and can be recovered from the culture medium or periplasm, and can be recovered from the culture medium or periplasm, and can be expected from the culture medium or periplasm, and an experience of most human-human ig are of M class, easily contained and aggregated, and these can now be changed to G, A or E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence - from pectate lyase to ensure transport of protein from the cytoplasm, esp. for prodn. of antibodies
                                                                                                                                                                                                                                                                                                                                                                          Improved prodn. of protein in Gram -ve bacteria using signal sequence - from pertate lyase to ensure transport of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; murine; human anti-hepatitis antibody; heavy chain; immunoglobulin fragment production; Ig fragment production; monoclonal antibody L6; human lung carcinoma cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%; Score 586; DB 18;
81.4%; Pred. No. 2.6e-41;
ive 5; Mismatches 17;
                                                                                                                                                                   Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human anti-hepatitis antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 12B; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W47510 standard; Protein; 136 AA
                                                                                                                                                                   Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0357234
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                                                                                                                                                                                                                                         WPI; 1997-011254/01.
N-PSDB; T51039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 114; Conserv
                                                                                                                                                              Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 AA;
                                                                               (XOMA ) XOMA CORP.
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.. 7

Job time: 119 sec

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The present sequence was used in the development of a novel method:

for the production of an immunoglobulin (Ig) fragment capable of

binding an antigen. The method comprises culturing an E. Coli host

that has been transformed with a nucleic acid molecule encoding the

culture that has been transformed with a nucleic acid molecule encoding the

culture that has been transformed with a nucleic acid molecule encoding the

culture that has been transformed with a nucleic acid molecule encoding the

culture to a DNA sequence encoding at least the variable region of

linked to a DNA sequence encoding at least the variable region of

culture to a single protactle; and (b) pectate lyase secretion signal sequence

operably linked to a DNA sequence encoding at least the variable

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain, where (a) and (b) are operably linked

credion of an Ig light chain; promoter to forms a produced by

chains an antibodies of production of the problem of class switching antibody molecules.

the problem of class switching antibody molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding secretable immunoglobulin fragments - comprising at least the variable regions of light or heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example II; Fig 12B; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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                                                                      95US-0467140
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85US-0793980
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88US-0142039
                                                                                                                                                                                                                                                                                                                                     92US-0987555
94US-0299085
                                                                                                                                                                                                                                                                                                                                                                                                               95US-0467140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Better M, Horwitz AH,
Wall R, Wilsox GL;
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N-PSDB; V18553, V18554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XOMA ) XOMA CORP.
                                                                      06-JUN-1995;
                                                                                                                                             29-MAR-1990,
01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                     08-DEC-1992;
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                                                                                                                                                                                                                           27-OCT-1986
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16-DEC-1997
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.; ? 1 MGWSCI1LFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60 4; Query Match 77.4%; Score 586; DB 19; Length 136; Best Local Similarity 81.4%; Pred. No. 2.6e-41; Matches 114; Conservative 5; Mismatches 17; Indels DGWDYAIDYWGQGTSVTVSS 140 d-w---faywgggtlvtvss 136 121 121 qq ò g ŏ ò

Search completed: April 13, 2001, 15:35:40

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Sequence 35, Appl
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Sequence 12, Appl
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APPLICANT: Ringler, Douglas J.
APPLICANT: Sewman, Walter
APPLICANT: Newman, Walter
APPLICANT: Bendig, Mary M.
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PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PTLING DATE: 15-AUG-1996
CLASSIFICATION: 43*
PTORNEX/AGRATT
ATORNEX/AGRATT

1 US-08-779-784-26
7 US-09-322-862-26
0 US-09-922-862-26
8 US-09-408-646-143
8 US-09-408-646-145
8 US-09-408-646-145
8 US-09-408-646-145
8 US-09-408-646-117
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8 US-08-921-060-113
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8 US-08-921-1178-35
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US-08-073-967-44
US-08-553-497-12
US-08-286-754-78
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NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 15, Application US/08700737 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
        Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Militia C
CITY: Lexington
STATE: Massachusetts
        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548.
     RESULT
                                                                                                                                                            April 13, 2001, 17:37:49; Search time 117.03 Seconds (without alignments) 192.426 Million cell updates/sec
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Sequence 4, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
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Sequence 9, Appli
Sequence 24, Appli
Sequence 24, Appli
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                                                                                                                                                                                                                                                                                                                                     1 MGWSCIILFLVSTATSVHSQ.........DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

9: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

12: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

15: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

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10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

22: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-700-737-15
US-08-700-737-4
US-08-700-737-2
US-08-700-737-9
US-08-700-737-19
US-09-053-583-9
US-09-053-583-9
US-09-499-666-9
US-09-499-662-9
US-08-692-084-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1009251 seqs, 160854530 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match
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Result Š

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        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     61 GGGLEWI(EIDPSESNINYNOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                            1 MGWSCIIIFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Singler, Douglas J.
APPLICANT: Singler, Douglas J.
APPLICANT: Gones, S. Tarran
APPLICANT: Gones, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Sendig, Mary M.
APPLICANT: Sendig, Mary M.
ATITLE OF INVENTION: INTEGRIN
TITLE OF INVENTION: INTEGRIN
TITLE OF INVENTION: INTEGRIN
                                                                                                                                                                                                                               Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington CITY: Lexington STATE: Masachusetts
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                                                                                                                                                                                                                               Score 757; DB 11;
Pred. No. 4.4e-65;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGE NT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE, DOCKET NUMBER: LKS95-10
TELECOMMUNIC ATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYFE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 140; Conservative 0;
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TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (517) 861-9540
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DGWDYAI)YWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DGWDYAII)YWGQGTSVTVSS 140
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
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CORRESPONDENJE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                    , MOLECULE TYPE: protein US-08-700-737-15
                                                                                                                                           linear
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                                                                                                                                          61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                               1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
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APPLICANT: Ponath, Paul D.
APPLICANT: Name, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF SEQUENCES: 63
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Length 137;
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                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.2%; Score 713; DB 11;
99.3%; Pred. No. 7.7e-61;
tive 0; Mismatches 1;
Score 730; DB 11;
Pred. No. 1.7e-62;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                     US-08-700-737-2; Sequence 2, Application US/08700737; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE COCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,
     96.4%;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            121 DGWDYAIDYWGQGTSVT 137
                                                                                                                                                                                                                         DGWDYAIDYWGQGTSVT 137
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                                          Conservative
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear US-08-700-737-2
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Best Local Similarity
                       Best_Local Similarity
Matches 135; Conserv
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83.9%;
86.7%;
                           Ponath, Paul D.
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APPLICANT: Ohsumi, Jun
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.7
Matches 117; Conservative
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APPLICANT: Shiraishi, Akio
APPLICANT: Yonehara, Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-19
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67 IGEIDPSESNTNYNQKFKGKATLTVDISSSTAXMQLSSLTSEDSAVYYCARGGYDGWDYA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ringler, Couglas J.
APPLICANT: Name of S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: Saldanha, Walter
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HURGRIN
MUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02173
ZIP: 02173
ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 425.5
                                                                                                                                                                                 Sequence 9, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION UNDBER: 22,592
REFERENCE/DOCKET UNDBER: LKS9:
TELEPHONE: (G17) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                         APPLICANT: Ponath, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
                                                                 127 IDYWGQGTSVTVSS 140
                                          127 IDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Lexington
STATE: Massachusetts
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US-08-700-737-9
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66 WIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDY 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 180;
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 635; DB 11;
Pred. No. 3.1e-53;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AuditER: IBM PC compatible
...emem: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS9:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
INFORMATION TO SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
INFORMATION ACIDS
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
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GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Ichikawa, Kimihisa
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSCIILELVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
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Pred. No. 7.8e-51;
                                                                                                                                                                                                                                                                               Score 615; DB 14;
Pred. No. 7.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Serizava, Nobufusa
APPLICANT: Hariyama, Hideyuki
APPLICANT: Hariyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTON: Anti-Fas Antibodies
TITLE OF INVENTON: Anti-Fas Antibodies
CURRENT APPLICATION NUMBER: US/09/408,646A
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: JP 10-276881
EARLIER PILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
       CARRENT FILING DATE: 1998-04-01
EARLIER APPLICATION NUMBER: JP HEI 9-82953
EARLIER FILING DATE: 1997-04-01
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ 1D NOS: 123
SOFTWARE: PATERIIN VET: 2.0
                                                                                                                                                                                                                                                                                                                 5; Mismatches
US/09/053,583A
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121 YSNNWY!DVWGTGTTVTVSS 140
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121 YSNNWYF;)VWGTGTTVTVSS 140
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illarity 84.3%;
Conservative
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Best Local Similarity 84.3%;
Matches 118; Conservative
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus US-09-408-646-9
                                                                                                                                                                                                                   ), ORGANISM: Mus musculus
US-09-053-583-9
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Best Local Similarity
Matches 118; Conserv
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                                                                                                                                                                                                        TYPE: PRT
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Retileborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Millen, White, Zelano & Branigan, P.C. 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,165 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                            Score 615; DB 18;
Pred. No. 7.8e-51;
5; Mismatches 17;
       Sequence 9, Application US/09499662
Sequence 9, Application US/09499662
Sequence 19, Application US/09499662
Septicant: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/09/499,662
CURRENT FILING DATE: 2000-02-09
CURRENT FILING DATE: 1998-04-01
SARLIER FILING DATE: 1998-04-01
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MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DGWDYAIDYWGQGTSVTVSS 140
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84.3%;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2'
Best Local Similarity 84.3'
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
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STREET: 22
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US-08-487-165-24
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LENGTH: 464
US-09-499-662-9
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61 GOGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08779784
GENERAL INFORMATION:
APPLICANT: ROdriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   ö
                                                                                                                                                                         Length 143;
                                                                                                                                                                                                                23; Indels
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                    Score 583; DB 10;
Pred. No. 2.4e-48;
5; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: ISH PC compatible
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCHWARE: Patentin Release #1.0, Ver
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: /US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1966
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                        121 DGWDYAIDYWGQGTSVTVSS 140
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    77.0%;
80.0%;
                        : 143 amino acids
amino acid
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amino acid
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Matches 112; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                           TOPOLOGY: Inear

MOLECULE TYPE: protein

US-08-692-084-26
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jerse
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US-08-779-784-26
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US-08-779-784-26
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GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MONOC NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GOGLEWIGEFNPSNGRINYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                            Score 589; DB 8;
Pred. No. 6.2e-49;
6; Mismatches 21
                                                                                 REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430C1
TELEPHONE: 703-243-6333
TELEFHONE: 703-243-6410
FELEEX: 64191
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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REFERENCE/DOCKET NUMBER: 1199-1-001 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,084
FILING DATE: 08-AUC-1996
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/236,520
FILING DATE: 29-ARR-1994
ATTORNEY/AGENT INFORMATION:
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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Best Local Similarity 80.7%;
Matches 113; Conservative
                                                                          NAME: Hamlet-King, Diana REGISTRATION NUMBER: 33,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: New Jersey
COUNTRY: USA
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TOPOLOGY:
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APPLICANT: Miller, David J.
APPLICANT: Pecse, Larry N.
TITLE OF INVENTION: HUMAN IGM ANTIBODIES, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: HUMAN IGM ANTIBODIES, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF PARTICULARLY IN THE CENTRAL NERVOUS SYSTEM
FILE REFERENCE: 1199-1-005
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                                                                                                                                                      GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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                                                                           1 MGWSCIIIFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                               APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Kospen, H.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of FILE REFERENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT APPLICATION NUMBER: US/09/698,705
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    Length 143;
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                                      23; Indels
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Pred. No. 2.4e-48;
Score 583; DB 11;
Pred. No. 2.4e-48;
5; Mismatches 23;
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CURRENT FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICAT: ON NUMBER: 08/779,784 PRIOR FILING DITE: 1997-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICAT:ON NUMBER: 08/692,084 PRIOR FILING Di.TE: 1996-08-08 PRIOR APPLICAT:ON NUMBER: 08/236,520 PRIOR FILING Di.TE: 1994-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09698705 GENERAL INFORMATION:
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Query Match 77.0%;
Best Local Similarity 80.0%;
Matches 112; Conservative
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
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US-09-322-862-26
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Best Local Simi.arity
Matches 112; Conserv
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US-09-322-862-26
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LENGTH: 143
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APPLICANT:
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GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HOMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7 TITLE OF INVENTION: HUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                        Length 466;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                  CTHER INFORMATION: sequence is chimeric mouse/human US-09-698-705-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
                                                                                                                                                                                                                                                                                    76.9%; Score 582; DB 20; ilarity 79.3%; Pred. No. 1.2e-47; Conservative 11; Mismatches 14;
    us 60/162,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-10-29
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617) 861-6240
                                                            2000-02-16
                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
PRIOR APPLICATION NUMBER: C
PRIOR FILING DATE: 1999-10-
PRIOR APPLICATION NUMBER: C
PRIOR FILING DATE: 2000-02-
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
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                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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us-08-700-737-55

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-09-408-646-143
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75.6%; Score 572; DB 11; Length 121; 86.0%; Pred. No. 2.2e-47; 1.ve 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 143, Application US/09408646A
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Kaori
APPLICANT: Tamaki, Tohru
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 990540/HG
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: UF 10-276881
EARLIER FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 143
LENGTH: 470
Query Match
Best Local Similarity 86.0%
Matches 104; Conservative
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US-09-408-646-143
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Query Match
74.9%; Score 567; DB 18; Length 470;
Best Local Similarity 77.1%; Pred. No. 3.3e-46;
Matches 108; Conservative 10; Mismatches 22; Indels

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Gaps

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121 DGWDYAIDYWGQGTSVTVSS 140 ò

Search completed: April 13, 2001, 17:37:49 Job time: 166 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                           OM protein – protein search, using sw model
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Run on:

April 13, 2001, 17:37:56 ; Search time 4.45 Seconds (without alignments) 54.611 Million cell updates/sec

US-08-700-737-15 757 MGWSCIILFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

7695 seqs, 1735856 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\* e 4 e e

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 11	10		2		=						Segment 51 Appl				Sequence 2, Appli		Sequence 11333, A	Sequence 19592		Sociones 1, Applit		- 6		ò	ģ	Sequence 5, Appli	Sequence 8, Appli
SUMMARIES	ID	US-08-475-815A-11	US-09-386-658-2	US-09-509-031-16	US-09-782-504-4	US-08-475-815A-7	US-09-509-031-11	US-09-509-031-6	US-09-509-031-4	US-09-739-449-9534	US-09-193-562D-28	US-09-739-449-12328	PCT-US01-09226-51	US-09-739-449-11638	US-09-814-950-4	US-09-814-950-2	US-09-386-658-4	US-09-739-449-11939	US-09-308-453-2	US-09-739-449-12522	US-09-706-029-1	US-09-739-449-11223	US-09-815-108-7	115-09-815-108-20	110 00 010 100 20	0-904-919-60 50	9-80T-CT9-60-SO	05-09-815-108-5	US-09-815-108-8
	DB	4	Ŋ			4																							S
	Ouery Match Length DB	140	132	482	240	128	155	342	495	442	914	517	753	281	170	172	109	757	1008	240	317	639	574	342	379	7	7 7	7/5	504
æ	Ouery	72.5	61.2	37.3	32.0	16.1	14.1	14.1	14.1	9.2	8.8	9.8	9.8	8.5	8.4	8.4	8.3	8.2	8.0	7.9	7.9	7.9	7.8	7.7	7 7			- 1	?;
	Score	549	463	282.5	242	122	107	107	107	69.5	99	65	65	64	63.5	63.5	62.5	62	60.5	9	59.5	59.5	59	58.5	58.5	 		9 6	0.90
	Result No.	7	ď	m	₹	ហ	9	7	ω,	ָּט פּ	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	30	9 6	7

US-08-475-815A-11

	Sequence 17, Appl		Sequence 2, Appli							Sequence 5. Appl t						
US-09-815-108-15	US-09-815-108-10	US-09-815-108-3	US-09-815-108-2	US-09-815-108-22	US-09-739-449-10479	US-09-739-449-10300	US-09-739-449-12898	US-09-810-264-26	US-09-739-449-8302	US-09-813-742-5	US-09-813-742-3	US-09-739-449-10936	US-09-809-391-481	US-09-739-449-11627	US-09-809-391-754	US-09-739-449-12644
φ	4 4	9	9	4 5	8	2 5	1 5	2 5	2	2	4	5	1 5	8	1 5	9
504	200	20	52	59	41	111	25	17	32	65	114	21	57	175	10	21
7.7	7.7	7.7	7.7	7.7	7.6	7.6	7.5	7.5	7.5	7.4	7.4	7.3	7.3	7.3	7.3	7.3
58.5	58.5	58.5	58.5	58.5	57.5	57.5	57	56.5	56.5	.56	26	55.5	55.5	55.5	52	22
28	90	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Sequence 11, Application US/08475815A
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: THERRAPETIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23522-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,030
REFERENCE/FOOCKET UNBER: 23;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-822-094
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 140 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
COUNTRY: US
ZIP: 20005
RESULT 1
US-08-475-815A-11
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Trautlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
COURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQGLEWI;EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGLEWICEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSCII.JELVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                   1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
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60
Length 140;
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                                     24; Indels
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APPLICANT: Chin, Bi-Xing
TITLE OF INVENTION: ANTHRODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JPW/SHS/MVM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEC ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
 ; Score 549; DB 4;
; Pred. No. 9.1e-51;
10; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 61.2%; Score 463; DB 5, Best Local Simi.arity 65.0%; Pred. No. 6e-42; Matches 91; Conservative 12; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09509031
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09386658 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DGWDYAI JYWGQGTSVTVSS 140
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------\YWGOGTLLTVSA 132
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                                                                                                                                                                                                               DGWDYAILYWGQGTSVTVSS 140
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        Query Match 72.5%
Best Local Similarity 75.7%
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: mouse [murine] US-09-386-658-2
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LENGŅH: 482
                                                                                                                                                                                                                                                                                                                   US-09-386-658-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                Gaps
CTHER INFORMATION: Description of Artificial Sequence:ccMTLgL protein corner in INFORMATION: sequence US-09-509-031-16
                                                                                                                                                                                     SQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESN 76
                                                                                                                                                                                                               8
                                                                                                        Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.0%; Score 242; DB 5; Length 240; 47.9%; Pred. No. 6.4e-19; ive 24; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,504
FILING DATE: 12-Feb-2001
CLASSIFICATION: CUNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bruce, Kim Folger
Schreiber, George J.
Siegall, Clay
McAndrew, Stephen
TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
CARCINOMAS
                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ROSENMAN Ph.D., Stephen J. REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 840065.405D3
                                                                                                        37.3%; Score 282.5; DB 544.4%; Pred. No. 9.8e-23;
                                                                                                                                                  27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karl Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONR: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09782504
GENERAL INFORMATION
GENERAL HELISTOM, Ingegerd
Hellstrom, Karl Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 240 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
                                                                                                      Ouery Match
Best Local Similarity 44.4%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.0
Best Local Similarity 47.9
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                      137 TVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                           149 TVSS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-782-504-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-782-504-4
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APPLICANT: Suess, dairiele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 PSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ASTRESGVPDRFSGSG-----SGTDFTLTISSLQAEDVAVYYCQQ-----YYSTPYSF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 VOLQOPGAELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
                                                                                                                                                                                                                                                                                     APPLICANT: Suces, Garlele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYIC ANTIBOIDES AND A METHOD OF PRODUCING SFILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein; OTHER INFORMATION: sequence
US-09-509-031-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: Kappa
protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.1%; Score 107; DB 5;
Best Local Similarity 27.3%; Pred. No. 3e-05;
Matches 35; Conservative 19; Mismatches 46;
                                                                                                                                                                                                                                 ; Sequence 11, Application US/09509031
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09509031; GENERAL INFORMATION: APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                       121 DGWDYAIDYWGQGTSVTV 138
                                                                                                                    --WTSNPPTFGGGTKLEI 127
                                                                                                                                                                                                                                                                         APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-509-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 GQGTKLEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 GQGTSVTV 138
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                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08475815A
GENERAL INFORMATION:
APPLICANT: Anderson. Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: THERAPEDITA APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                         20 QVOLQOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                             28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
16.1%; Score 122; DB 4;
Best Local Similarity 26.8%; Pred. No. 6.8e-07;
Matches 37; Conservative 28; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23522-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILLSBURY WINTHROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 2352
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-475-815A-7
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RESULT 10
US-09-193-562D-28
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Sequence 9534, Application US/09739449

Sequence 9534, Application US/09739449

GENERAL INFORMATION:
APPLICANT: HINKLE, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

PRIOR PEDICATION NUMBER: US 09/514,000

PRIOR FILING LATE: 2000-12-19

PRIOR FILING LATE: 2000-02-23

NUMBER OF SEQ ID NOS: 13351
                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NCHILLY, FIGURE M.
APPLICANT: SQUISS, GABIELE M.
APPLICANT: Tailinton, David M.
APPLICANT: Tailinton, David M.
APPLICANT: Tailinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICANTON NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SSCTUMARE: PATEILIN Ver. 2.1
SEQ ID NO 4
LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 PSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PSESNIN NOKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDY-W 130
                                                                                                                                                                                  32 VMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNY-LAWYQQKPGQPPKLLIYW---- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 VQLQQPGAELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
                                            Gaps
                                                                              -YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
                                                                                                            32 VMTQSPDi:LAVSLGERATINCKSSQSVLYSSNSKNY-LAWYQQKPGQPPKLLIYW----
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                                          28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Score 107; DB 5; Length 495; 27.3%; Pred. No. 0.00011; tive 19; Mismatches 46; Indels
Length, 342;
                                          46; Indels
Query Match
Best Local Similarity 27.3%; Pred. No. 7.4e-05;
Matches 35; (onservative 19; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                  US-09-509-031-4; Sequence 4, App.ication US/09509031; GENERAL INFORMATION:
                                                                                    21 VQLQQPGLELVKPGTSVKLSCKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koentgen, Frank
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nes 35; Conserv
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                                                                                                                                                                                                                                                 131 GQGTSVT" 138
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Matches
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US-09-139-449-12328
US-09-139-449-12328
Sequence 12328, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewn C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-02-23
SEQ ID NO 12328
LENGTH: 517
                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                      86 KATLTVDISSSTAYM----ARGGYDGW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 LW----DPS------GOKOGG---FVVDKNTKMAYLQIPGIAKVGT------WK 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 EWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWD 124
                                                                                                                                                                                                                                                                                     97 AILPOPGLLADLAAKGFLVPLGDDTAKWVEENYGAGKSWVDLGSYKGKDGNKAY-FAFPF 155
                                                                                                                                                                                                                                                                                                                                                                                 KA----DVKSLVWYVPENFERAGYKVPESMEDLLKLTDQIVADGGTPWCIGLGSGGATGW 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VSTATSVHSQ--VQLQQPGAELVKP----GTSVKLSCKGYGYTFTSYWMHWVKQRPGQGL 64
                                                                                                                                                                                                                                    28 AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNTNYNQKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/09193562D
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
Activated Chloride Channel-Adhesion Molecules
FILE REPRESENCE: 18617.0052
CURRENT APPLICATION NUMBER: US/09/193,562D
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US/60/065,922
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 914;
                                                                                                                                          Length 442;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 66.5; DB 5; 25.0%; Pred. No. 3.4;
                                                                                                                                          5;
                                                                                                                                        ; Score 69.5; DB
; Pred. No. 0.72;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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; LENGTH: 442
TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534
                                                                                                                                             9.2%;
                                                                                                                                        Query Match
Best Local Similarity 25.08
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.8%
Best Local Similarity 25.0%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 YAIDYWGQGTSVTVSS 140
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; ORCANISM: Agrobacterium tumefaciens US-09-739-449-11638
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
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US-09-739-449-11638
Sequence 11638, Application US/09739449
Sequence 11638, Application US/09739449
Sequence 11638
Sequence 11638
Sequence 11638
Sequence 11638
Sequences and Uses Thereof
TTPLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
TTPLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
CURRENT PELLING DATE: 200-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 11638
LENGTH: 281
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                                                                                                                                                                                                                           58 QRP------GQGLEWIGEIDPSESNTNYNQKFKG---KATLTVDIS-SSTAYMQLS 103
                                                                                                                                                                                                                                                    57 RVEIQRAG----EWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNL 112
                                                                                                             Gaps
                                                                                                                                         12 STATSVH--SQVQLQQPGAELVKPGTSVKLSCK----GYGYTFTSYWM-----HWVK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQPGAELVKPGT----SVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEI 70
                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                    Length 517;
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                                                                                                           41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                      104 SLTSEDSA-----VYY-----CARGG-----YDGWDYAIDYW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                            Query Match
8.6%; Score 65; DB 5;
Best Local Similarity 24.7%; Pred. No. 2.5;
Matches 41; Conservative 22; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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8.6%; Score 65; DB 1
Best Local Similarity 24.7%; Pred. No. 3.9;
Matches 21; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SMITHKLINE BECHAM CORPORATION
APPLICANT: SMITHKLINE BECHAM CORPORATION
TITLE OF INVENTION: NUMBER: COMPOUNDS
FILE REFERENCE: GF50018
CURRENT APPLICATION NUMBER: PCT/US01/09226
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
SPRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FASTSEO fOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 SCSGTEQSVTECASRGWGNSDCTHD 137
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PCT-US01-09226-51
US-09-739-449-12328
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PCT-US01-09226-51
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LENGTH: 753
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Sequence 4, Application US/09014950
GENERAL INFORMATION:
APPLICANT WET, MIG-Hui et al
APPLICANT SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT APPLICATION NUMBER: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09814950
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOll14
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTERE FASTERE FOR WINDOWS VETSION 4.0
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                                                                                                         43 GYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQL 102
                                                                                                                                                90 GVGYQFNNYF-----RSDVTLDYMGKSDFRGSTSGFCGSVPGRC-VSADLSSLSAYTLM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTN 78
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59 TKYQISQPEVYVAAPGESLEVRCLLKDAAVISWTKDGVHLGPNNRTVLIGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.4%; Score 63.5; DB 5; Length 170; 20.6%; Pred. No. 0.98; 1ve 11; Mismatches 37; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 172;
           Length 281;
                                                             Indels
                                                          35;
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Query Match
8.5%; Score 64; DB 5;
Best Local Similarity 25.8%; Prad. No. 1.6;
Matches 23; Conservative 17; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 YNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YLOIKGATPRDSGLYAC 126
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Pred. No. 1;
                                                                                                                                                                                                                103 SS----LTSEDSAVYYCA---RGGYDGWD 124
                                                                                                                                                                                                                                                     8.4%;
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Best Local Similarity
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

April 13, 2001, 15:36:11 ; Search time 28.17 Seconds (without alignments) 95.475 Million cell updates/sec Run on:

US-08-700-737-15 757 Title: Perfect score:

1 MGWSCIILFLVSTATSVHSQ.......DGWDYAIDYWGQGTSVTVSS 140 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

185757 seqs, 19210857 residues Searched:

Total number, of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptcdata/2/laa/5A\_COMB.pep:\*
/cgn2\_6/ptcdata/2/laa/5B\_COMB.pep:\*
/cgn2\_6/ptcdata/2/laa/6A\_COMB.pep:\*
/cgn2\_6/ptcdata/2/laa/6B\_COMB.pep:\*
/cgn2\_6/ptcdata/2/laa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptcdata/2/laa/PcTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	9	9 Query	44	ć	SUMMARIES	
2	2000	Match	match Length	3 :	ID	Description
<b>н</b> (	297		464	~	US-08-353-400-36	guence 36.
7	589		140	-	US-07-946-421-24	770
m	583	77.0	143	٦	US-08-236-520-7	
4	583	77.0	143	Ŋ	PCT-US95-05262-7	
ហ	544.5	71.9	139	Н	US-08-137-117D-35	Sequence 7, Appli
9	544.5	71.9	139	~	US-08-436-717-35	, ה ה
7	541	71.5	140		US-08-476-275-6	) )
80	536	70.8	119	(7	US-08-553-497A-12	5
o i	532	70.3	138	Н	US-08-482-882-78	
10	532	70.3	138	~	US-08-483-389-78	ā
11	532	70.3	138	~	US-08-487-113D-78	òa
12	532	70.3	138	~	US-08-473-503-78	Segmence 78 Appl
£ ;	532	70.3	138	7	US-08-483-932-78	78,
14	533	70.3	138	~	US-08-720-420A-78	ά
15	532	70.3	138	m	US-08-714-017-78	2 0
16	532	70.3	138	٣	US-08-475-680-78	-
17	531	70.1	136	'n		
18	527.5	69.7	139	П	US-08-253-877C-8	èα
19	527.5	69.7	139	~	US-08-452-164A-8	α
50	526.5	9.69	138	ന	US-08-603-024-2	
21	524	69.3	119	m	US-08-881-037-62	, 5
22	21.	68.8	269	~	US-08-428-257A-72	Sequence of Apple
23	21,	68.8	269	~	US-08-491-988-3	,
24	21.	68.8	402	~	US-08-491-988-9	
22	21.	68.8	415	2	115-08-491-988-7	ņ
56	521.5	68.8	435	~	-08-491	Sequence /, Appli
27	20.	68.8	122	Н	-08-236-520-	ò c
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Sequence 9	Trade o conceptor	Tride to some of	Seducince 33, Appl	Sequence 61, Appl.	Sequence 63. Appl	Section 11 aprendictions	, ,	- r	Seducince / Appril	Sequence 34, Appl	Segmence 12 Appl	Sequence 12 April	4 -	sednence for, App	Sequence 101, App	101	Sequence 101 App	מלע ידמד שיוויים	Sequence 101, App	Sequence 60. April	Sequence 6, Appli
PCT-US95-05262-9	US-08-553-497A-8	118-08-353-400-33	10 - 100 - 00 - 011	19-160-188-80-CO	US-08-881-037-63	PCT-US93-11611-11	US-08-303-569B-7	115-08-116-247-7	7 0 0 0 0 1 1 1 0 0 0 0 1 1 1 1 1 1 1 1	US-US-213-908-34	US-08-579-378A-12	PCT-US93-11612-12	119-07-634-77-11	TOT 0/9 #00 /0 00	US-U8-4/7-728-101	US-08-474-040-101	US-08-487-200-101	101 102 107 07 01	TOT-/6C-888-90-60	US-08-881-037-60	US-08-767-128-6
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122	119	445	110	113	119	136	468	468	15.1	1 1	140	140	152	1 (	707	. 152	152	153	707	119	119
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28	29	30	31	1 6	35	33	34	35	36	2 5	3/	38	39		<b>?</b> :	41	42	43		44	45

## ALIGNMENTS

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SOFFWARE: Datentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN 1994
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LEGISTH: 464 amino acids
TYPE: amino acids
STRANDENNES: single
                                                                                                                     TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   Sequence 36, Application US/08353400 Patent No. 5665357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-36
                                                                                 GENERAL INFORMATION:
KESULT 1
US-08-353-400-36
                                                                                                    APPLICANT:
                                                           ; Patent No.
```

Gaps ö 78.9%; Score 597; DB 1; Length 464; 80.0%; Pred. No. 3e-47; Live 11; Mismatches 17; Indels Ouery Match Best Local Similarity 80.0% Matches 112; Conservative

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121 DGWDYAIDYWGQGTSVTVSS 140 δ

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MONOCLONAL ANTIBODIES WHICH PROMOTE CENTRAL NERVOUS SYSTEM REMYELINATION
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
                                                                                                                                                                                                    COMPUTER REALBLE FORD

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE PATENTIN PC PC DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/236,520

FILING DATE: 29-APR-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REFIRENCE/DOCKET NUMBER: 27,227

REFIRENCE/DOCKET NUMBER: MAV92-01

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAX: 617-861-6240

TELEFRAX: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 583; DB 1;
Pred. No. 1.4e-46;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YYGSRNFDYWGQGTTLTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                 Lexington
Massachusetts
                                                                                                                                                                     ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Matches 112; Conserv
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                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
PCT-US95-05262-7
                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-236-520-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSCIIJFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.8%; Score 589; DB 1; Length 140;
80.7%; Pred. No. 4e-47;
Live 6; Mismatches 21; Indels
                                                                                                          APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Kettleborough, Catherine A. APPLICANT: Saldanha, Jose TITLE OF INVENTION: Humanized and Chimeric Monoclonal TITLE OF INVENTION: Antibodies CORRESPONDENCE: 42
                                                                                                                                                                                                                                       P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421 FILING DATE: 06 NOV-1992
                                                                                                                                                                                                                                       2: Millen, White, Zelano & Branigan, 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DATE:
PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: Ham.et-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/POCKET NUMBER: 33,302
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING :YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08236520 Patent No. 5591629 GENERAL INFORMATION:
                                                   Sequence 24, Application US/07946421 Patent No. 5558864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DGWDYAIJYWGQGTSVTVSS 140
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DYDGRYFDYWGQGTTLTVSS 140
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Miller, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 1.10 amino acids
amino acid
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Best Local Similarity 80.7'
Matches 113; Sonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
                                                                                                                                                                                                                                                   STREET: 2200 CTTY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22201
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
US-07-946-421-24
                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-236-520-7
                   RESULT 2
US-07-946-421-24
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                              1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                              Sequence 7, Application PC/TUS9505262
Sequence 7, Application PC/TUS9505262
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hamilton, Brook, Smithy & Reynolds, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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61 GHGLEWIGEILPGTGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCASLDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, KAD
APPLICANT: SATO, KAD
APPLICANT: SALOS, Mary
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.9%; Score 544.5; DB 1
Best Local Similarity 72.9%; Pred. No. 4.7e-43;
Matches 102; Conservative 13; Mismatches 24
                                                                                                                                                            53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
RICHARDA PAPLICATION DATA:
ARPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D. COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~ETEM: TEM PC Compatible
~~ETEM: PC COMPATIBLE
~~ETEM: PC COMPATIBLE
                      PRIOR APPLICATION DATA.

APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/08436717 Patent No. 5817790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SGY-YAMDYWGQGTSVTVSS 139
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-137-117D-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-436-717-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 583; DB 5; Length 143; Pred. No. 1.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, SLEVEN
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-DEC-1993
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFRENCE/POCKET NUMBER: MAY92-01 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-861-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-137-117D-35; Sequence 35, Application US/08137117D; Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YYGSRNFDYWGQGTTLTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                    TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERIZES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                       LENGTH: 143 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein
PCT-US95-05262-7
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Gaps

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APPLICATION.
FILING DATE: 17-NOV-100-1
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
TO DATE: 16-MAR-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: RETLIEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
                                                                                                                   REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 01.
                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DGWDYAIDYWGQGTSVTVSS 140
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                                                                                                                                                                                                    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   LENGTH: 140 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 105; Conservative
                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-476-275-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Reff, Mitchell B.
Rastetter, William H.
VINTION: Therapeutic Application of Chimeric and
VINTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
VINTION: Differentiation Antigen for the Treatment of B-Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GHGLEWIJELLPGTGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYCASLDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQGLEWI; EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGWSCII. FLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.9%; Score 544.5; DB 2; Best Local Simi.arity 72.9%; Pred. No. 4.7e-43; Matches 102; Conservative 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 639 Prince St. CITY: Alexandria
                                                                                                                            NAME: WEGHER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/HOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPAN: 202,672-5309
TELEFAX: 202,672-5399
APPLICATION NUMBER: JP 4-32084
FILING DATH: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATH: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGHER, HAROLD C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING 3YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08476275 Patent No. 5776156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson, Darrell R.
                                                                                                                                                                                                                     TELEX: 90.136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DGWDYAINYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SGY-YAM)YWGQGTSVTVSS 139
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Leonard, John E.
                                                                                                                                                                                                                                                                                                                   : 139 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPN: protein US-08-436-717-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JSA
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-275-6
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ANSEL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: ADAN, JAUME
APPLICANT: ROSEL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTI-EGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17.NOV-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.5%; Score 541; DB 1; 75.0%; Pred. No. 9.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
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Sequence 78, Application US/0848389
Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
ITILE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STARE: Illinois
COUWTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/009,266 FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYXCARSDYGSSHF--DYWGQGTTVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/08482882
Patent No. 5773218
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 66066
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 536; DB 2;
Pred. No. 2.3e-42;
4; Mismatches 12;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.8%;
85.1%;
                                                                                                                                                                                                                                                                                                                                    LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.1'
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-553-497A-12
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                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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STATE: Illinois
COUNTRY: USA
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1 MGWSCIILFLVSTATSVHSOVOLOOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
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            FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTOKNEY AGENT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISTATION NUMBER: 35,3022
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 3177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:
LENGTH: 138 antho acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 103; Conserva
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGGLEWIGYINPNTDYTEYNÖRFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARWG- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemāy
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 1111nols
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Rest Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                PRIOR APPLICATION DATE:

PRIOR APPLICATION DATE:

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-UN-1992

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 3744

TELECOMMUNICATION NUMBER: 32744

TELECOMMUNICATION NUMBER: 32744
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APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-473-503-78
; Sequence 78, Application US/08473503
; Patent No. 5869262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 138 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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Pred. No. 6.5e-42;
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STREET: (300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Patent No. 5837822
GENERAL INFORPATION:
APPLICANT: Vazeux, Rosemay
APPLICANT: Vazeux, Rosemay
TITLE OF INFURION: ICAM-Related Materials and Methods
NUMBER OF SIQUENCES: 120
CORRESPONDERCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061
FILING DATH: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATH: 26-MAY-1992
PRIOR APPLICATION DATA: 26-MAY-1992
FILING DATH: 27-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATH: 27-JAN-1992
ATTORNEY-AGENT INFORMATION:
NAME: Suh Young J. REGISTRATION NUMBER: P-41,337
REFERENCE, NOCKET NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAM: 312) 474-6340
TELETAX: 312) 474-6448
TELETAX: 312) 474-6460
INFORMATION FOX SEQ ID NO: 78:
SEQUENCE CHA ACTERESTICS:
LENGTH - 18
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
ZIP: 606(.6-6402
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APPLICATION NUMBER: US 08/102,852
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WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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llarity 73.6%;
Sonservative
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amilo acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 103; Conserva
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYP3:
US-08-483-389-78
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Patent No. 5880268
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SCOUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 532; DB 2; Length 138;
Pred. No. 6.5e-42;
6; Mismatches 29; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                        FILING DAYLE: US-AUG-1223
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: 37-302
ATORNEY/AGENT INFORMATION:
NAME: NO. 5869262and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELECHHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
                                      08/102,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/483,932
APPLICATION NUMBER: 08/286,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
70.3%;
Best Local Similarity 73.6%;
Matches 103; Conservative
                   FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 00
                                        MBER: US 06
05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-473-503-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Search completed: April 13, 2001, 15:36:11 Job time: 129 sec
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US-08-714-017-78
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Patent No. 604C176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: (300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPL: CATION DATA:
APPLICATION NUMBER: US/08/720,420A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 532; DB 2;
Pred. No. 6.5e-42;
6; Mismatches 29.
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATH: 26-Jan 100

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATH: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION TORORATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
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TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
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TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
                                                                                                                                             FRION APPLICATION DATA

PRIOR PAPLICATION DATA:

FILING DATH:

OP-JUN-1995

PRIOR PAPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754

FILING DATH:

APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

FILING DATH:

APPLICATION NUMBER: US 08/102,852

FILING DATH:

APPLICATION NUMBER: US 08/102,852

FILING DATH:

APPLICATION NUMBER: US 08/102,852

FILING DATH:

APPLICATION NUMBER: US 08/103
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73.6%;
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                                                                               FILING DATH:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 103; Conserv
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STREET: (300
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US-08-714-017-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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61 GOGLEWIGEIDPSESNTNYNOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Indels
                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714.017
FILING DAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 532; DB 3;
Pred. No. 6.5e-42;
6; Mismatches 29;
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
PRIOR APPLICATION NUMBER: US
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-UN-1992
PRIOR APPLICATION NUMBER: US
FILING DATE: 26-MAY-1992
FILING DATE: 26-MAY-1992
FILING DATE: 27-JAN-1992
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION
NAME: NO. 6040176 and, Greta E.
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37178
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.3%;
Best Local Similarity 73.6%;
Matches 103; Conservative
                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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